

[illegible]

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRGTGQEL
KEAALEPSMEKIFKIDQMGRWFFVAGGAAVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCGCCGCTCTCGGCCCTTCTGCAT
CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTTCGGGAGCGCGCGCGCTGCGAGGG
GGTCGGCAGCGGGAGTCGGGCGGCTTGTGCATCTTGGCTACCTGTGGGTGCAAA**GATG**TCGG
ACATCGGAGACGTGGTTCAGGAGCATCCCGGCGATCACGGCGCTATTGGTTCCGCGCCACCGCTC
CGCGTGGCCCTTGGTCGGCAAACTCGGCCCTCATCAGCCGGCCCTACCTCTTCCCTCTGCGCCGA
AGCCTTCCCTTTATCGCTTTTCAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCCTCTGGT
GTCCAGGAACCTGGATTCTTTTATTGGTCAATTTATATTTCTATATCAGTATCTTACGCCA
CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTATTCATGCTCCTCTTTAACTG
GATTTGCATCGTGAATTAAGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA
TGTCACTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGATTGTATCACTTTTGGTTTGG
ACACGATTTAAGGCCCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTAIATCATCGGAGG
CTCGGTATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTCTTAATGTTCA
GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCCCTGG
CTGCCAGTAGGAGAGAGGAGATATCAGGATTTGGTGTGCCCTCTGCTAGCATGAGCGGAGC
TGCTGATCAGAATGGCGGAGGCGGGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC
AGT**GAA**GGGGCGGCCCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCTCCAGTCTGGGTG
CACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCAGCTGAATGTAGCTCTTTC
AGCTCAGAGACAAGTTTCTTAAATCCCGAAGAAAATTAAGTGTTCACAGTTTTCAGGAT
TGTCAATTAAGTCTCTTACGCTGTGAAGAACAATAACCACTGCGAATTCGCAAACTGAC
TACATTTTGTGTCTTCTCTCTCCCTTTCCGTCGTAATAATGGGCTTTAGCGGGTCTT
AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAAACCTTCCCAAAAGGACCTTATCTCTT
TCTTGCAACATGCGCTCTCTCCCACTTTTCCCAACCCCACTTTGCAACTAGAAAAAGTTG
CCCATAAAATTTGCTCGCCCTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGTC
ACAACAATCATATTACGTTATTTTCCCTTTTGGTGGCAGAAGCTTTACCAATAGGGGGAG
AAGACAGCCACGGATGAAGGCTTCTCAGCTTTTGGAAATTCGCTCGACTGACATCCGTTGTT
AACCCTTTGCCACTCTTCAGATATTTTTATAAAAAAAGTACCACCTGAGTCTAGAGGCCA
CAGATTTGGTTATTAAATGAGATACGAGGTTGGTGCTGGGTGTTTGTTCCTGAGCTAAGTGA
TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC
TTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTGCTTTGTGT
TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG
ATTCCCATTTCAATCTCATTTCTGGATATGTGTTTATGAGTAAAGGAGGAGAGACCCCTATA
CGCTATTTAAATGTCACTTTTTTGCCATATCCCCGTTTTTTTGGTCACTTTTCAATTAATGT
GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCAACATCTA
AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGAAGGTTGTGTTA
TTTTGAGTCAATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTT
TCGTAGGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAAAATAAGTTTTTTGAAAGCCA
TGGCTTTTCACACAGCTATTTTTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
ATTGAGTGGCTGTCACTTTTGGGCAACTAAAAAGGCTTCAAAACGTTTTGATCAGTTTCTT
TTCAGGAACATTTGTGCTCTAACAGTATGACTATTTTCCCCCACTTCTAAACAGCTGTGAT
GTGTGTTATCCTAGGAAATGAGAGTTGGCAACAACCTCTCATTTTGAATAGAGTTTGTGTG
TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGCTGGAACCTTAACTGTCA
TGTTTTGTGTTCATCTGTGGCCACAATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT
CCAATTATGTTGCACGTACACTCATTTGTACAGCGGTGGAGACTCATTTGATGTATGAAGAATA
TTTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCCTTTACCAGTCAGCTGCCTGCGAG
CAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAATTTTTCAGTCTCAGGGCAAAATGTT
ATGAAGTTATTTCTCTTAAACATGGTTAGGAAGCTGATACGTTATTGATTTTGTCTGGATT
ATGTTCTCGGAATAATTTTACCAAAACAAGCTATTTGAGTTTTGACTTTGACAAAGGCAAAACA
TGACAGTGGATTCTCTTTACAAATGAAAAAAAATCTTTATTTTGTATAAAGGACTTCCC
TTTTTGTAACATAATCTTTTTTATTTGGTAAAAATGTAAATTAAGTGCACCTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWCIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCCGGCTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCTCGGGGCTGAGCGACTGCGGGGCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCTGTGCC
 CCTTGTGGGGCGGCA**TTGG**CTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTCCCTTGTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAGAGATGAAAATCCT
 GAGGGAAGTTCTTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGGAAAA
 AACAGTTATCAGAGGCTAAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTCCCAAGGGGATGGTGAACATTTTGACACCCACCCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCCTTTGGGAAGAAAAGTGGAAGGTCTGAAACTTCTCCCTCC
 CACAAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAGAAGCTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAACTCAAAGAAGAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEESKLTYTEIHQEYKELVEKLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMLQAIRIIQERNGLVPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

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FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAA

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FIGURE 8

GCGTGGTTTTTGTCTGCAATAGCGGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTCGGTCTTCTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAATAAAC
 AGTGGAAATGGAAAAACAGTGCCTGTAGTCATCCTGTAATATGCTCTTGTCAACAATGTATAC
 ATTCTGCTAGGTGCCATATTCTATGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAACAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTCTGTGTGCATCTGTGTTATAAAGAAAGATCATCAAAAGTAG
 AAATTTGAAATATGCTTCCTGGAAGGAATTTCTCTGATTTTCATGAAGTGGTCCATTCTCGCT
 TCTTTATTTCTCGGATAACTTGATTGCTTCTATGTCTCTGTCTTACTTCAACCAGCCATG
 GCTTTTATCTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGCTGAA
 GAGGCGCTCAAACCTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC
 TTTTTACGCCCTTCCAATTTCTGCTTCTTTTTCAGAAGTGAGTGTCCAGAAAAAGACAATTG
 TACAGCAAAGGAATGGACCTTTTCTGAAGCTAAATGGAACACCCAGCCAGAGTTTCTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAAAGATACTGAAGGAGGGGAACCACTACTGAAAGCATCTTTCATACA
 GAACAGCAAACTCTATTCTTTGGCATCTGTTTAAATGGGCTGACTCTGGGCTTTCAGAGGA
 GTAACCGTGATCAGATTAGAAGCTGTGGATTTTTTATGGCCACAGTGCATTTTTCAGTAGCC
 CTTATTTTTGTAACTGCATTCCAGGGCCTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCAGTGTCTTGATGGCCAGGTACCAGTCTCATTTACACAACAGTGTCTGTCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCCATCAGTCTTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCACATAGTTTGCA
 GCTCTCTTGAACCTTATTTTTACATTTTCAGTGTGTTGTAATATTATCTTTTCACTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGATATATCTAGTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCTAAGAAGCTGATACAGGAGTAACA
 ATATGAAGAAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTTGTAAATATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT
 TCTCCCTTTTAAACATTTATAAAGCTAGGTTGTCTCTGAATTTTAGGGCTTAGAGATAGT
 CATTTTGAAGCTAAGAGGAGCAACGGGACCCCTTCTAAAACGTTGGTTGAAGGACCTTAATAC
 CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAAATATTGCTGAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAAATTTTGAAGAAATTCATGGGAAATGGATTTTTGT
 AATAATCTTTTGATGTTTTAAACATTTGGTTCCCTAGTACCATAGTTACCAGTTGTATTTTA
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAACTTTGAT
 GTCATTACTCTGAATATTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC
 CAGATTGTCAGTGAAGCTGATGCTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAAAACATGTTGACTTTTAACTGATGATGAATATTAACTACTCAAAAATAGAAAGACC
 AGTAATATAAAGTACCTTTACAGTGCTACTTCACACTTAAAGTGCATGTTATTTTCTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAAAACAAAGGTGACTTGCTCAGGCTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAAGTGGCAGGCTGTATGTTTACAGACTACCATACTGTAAATATGAGCTTATGGTGT
 CATCTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGTAATATACATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAAATTG
 GTGGAAATTTGTAATTAATAATATTATAAACCCT

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FIGURE 9

MEKQCCSHPVICSLSTMYTFLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQ PAMAV
 IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCTCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAACCTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGGCTTGGCTAGCGCGCGGCGGCG
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGCGAGGAGCAT
 CCCGTCTACCAAGTCCCAAGCGGCGTGGCCGCGGGTTCATGGCCAAAGGAGAAGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCGCCGGCCCA
 GGTGAAGAAAGAACCGAAAGAAAGAAACAACAGTTGTCTGTTTGCACAAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC
 CTATTG**CATG**CTGGGCTCAGGTGGGCCCCCTTCTCTGCCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTCGCCTTATGCCCTGGATCATCTTCTCCACGCCCCCTGGCCGCTATTGCCCTACTTCCTC
 ATCTGGTTCGTGCCCCGACTTCCCACACGCGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAACAATGGTCACTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGACGCGGATCCAGGACAAATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACACATGGCACCACTTCACAC
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGCTCATTGTCTGTATCTATATAAATCTG
 TGCTGTCTCCTGATCCTGGGCGTGCGGGAGCAGAGAACCCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCATACATCAAACCTT
 ATTACTGGCTTCTCTTCACTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTTGCTTTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCCTTCTTAC
 TACCTGGTCCATGCTGCCGTGATGTCTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCTCTATGTCTTCTTACCAGTTTGGCTCTGGAGTGTCT
 ACTGGGCATTTCTACCTCAGTCTGGACTTTGCAAGGTACAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCCATGTATGAGGAGAGGCGGCGGAGAAAGAA
 GGCCCTGCAGGCACTGAGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCT**TAG**GGCCCCGCCAGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGCTTGTCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGTGTGCTCACTGTGGGCGCGGCTGCTCTG
 TGGCCTCTGCTCCCTCTGCTGCTGCTGTGGGCGCAAGCCCTGGGCTGCCACTGTGAATA
 TGCCAAGACTGATCGGGCTAGCCCGGAACACTAATGTAGAACCCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAAATTTTCATAAAGCTGGAAAGC

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FIGURE 12

MWLRWALS LPPSSCLWAE PGMFSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSH TARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHHTGTTSHRETQKAYLLAAGVIVCIYIIICAV
ILILGVREQREPYEAAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNL LLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL
QALRDEASSSGCSETDSTELASIL

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GGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGC GGAGCAGAGAACCCATGAAGCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCTACGGCTGGTCATGAGCCAGGCCATACATCAAACCTTA
TTACTGGCTTCTCTTACCTCCTTGGCTTTTCATGCTGGTGAGGGGAACTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATATTACATATCGGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCTCTGGTCCATGCTGCTGATGTATTGACGACTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAAACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTCTGGAATACTGAGTTGTTTAGG
 ACTTTCTATTGTGGCAAACCTTCAGAAAAACAACCTTTTTGCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCCTACCAAATG
 CAGCCCAAAATCCATGGCAAACAAGTCTTCCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTGCATTTTCCTTCTTTGGTTTTTCCTGACTTACATTCTGTA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCTCTATGACACTG
 CACCTTGCCCTATTAAACAATGAACGAACACGGCTACTTTCCAGAGATATTTGAATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATCTTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACCTTTTTTATCTCAGAAAAATAAAGTCAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT YIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

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CGSAGCGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAATCAGCGGTCTAATTAAATCCTCTGGTTGTGTAAGCAGT
TACCAAGAATCTTCAACCCCTTCCCACAAAAGCTAATTGAGTACACGTTCTGTGAGTACA
CGTTCCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAAACAGAAACCTGTTAGAAATGTGGTGGTTTCAGCAGGCGCTACGTTTCCCTCCT
TCAGCCCTTGTAATTGGACATCTGCTGCTTTCATATTTTCATACCTAGTTCAGTAAACACT
CCACCATATAGACCCTGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCCGCGCTGCGTCCCGAGTGCAGTGTGCTTCTCGGTGCCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCCGCTTCTCGGCCTCCTTCTGGTCTTTCGCGGCTGCAC
 CTTGCGCTTGTACTTGTCTGTCGACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT
 TGTTCGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTCATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACATGATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTGGTCTCTAAAGCCCCCTATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTGAAGGTGTATTACATCAGGT
 TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCCTCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCACGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTCT
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

MRPLLGLLLVFAGCT¹ALYLLSTRLPGRRLGSTEEAGGRSLWFP²SDLAELRESEVLREYR³
KEHQAYV⁴FL⁵LCF⁶GAYLYKQGF⁷AI⁸PGSSFLNVL⁹AGALF¹⁰FWLGLLLCCV¹¹LT¹²SVGATCCYLL¹³SS¹⁴
IFGKQLVVSYP¹⁵FDK¹⁶VALL¹⁷Q¹⁸RKVEENRSL¹⁹FF²⁰FL²¹FL²²RF²³PM²⁴T²⁵N²⁶W²⁷FL²⁸NLS²⁹APIL³⁰NI³¹PV³²Q³³FF³⁴
F³⁵SVLIGLIPY³⁶NI³⁷FCV³⁸Q³⁹T⁴⁰GISL⁴¹TL⁴²SL⁴³DAL⁴⁴FSW⁴⁵DT⁴⁶V⁴⁷FKLLAIAM⁴⁸VALI⁴⁹PTGLIKK⁵⁰FS⁵¹Q⁵²KH⁵³L⁵⁴Q⁵⁵
LN⁵⁶ET⁵⁷STAN⁵⁸HN⁵⁹SR⁶⁰K⁶¹DT⁶²

Signal peptide:

amino acids 1-17

amino acids 101-123, 189-211

amino acids 172-176, 250-254

amino acids 240-244, 261-265

amino acids 13-19, 104-110, 115-121, 204-210

amino acids 27-31

amino acids 4-15

amino acids 25-31.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCGAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTTCCGAAGTCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACC
 CCCCCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTTGTGCCAGTACCCTGAGGCGACAGAAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCCATTTCCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCCTGTTTTCCTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAACTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCGAGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAA

MDLAANEISIDYDKLSITVDLVRQTGHQCGMSEKATEKFIHQLLLEKNEFQRPPFPQYPLLIIVVY
KVLATLGLILLTAYFVFIQPFSPLAPEPVLSGAHTWRSLLHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEFIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFAKWWRCFIERWFPPFPWRRLNRSQMLRELFPV
FTHLPFGKDSALNCKSLFHPFVGVSGMKMHKMDLFIISGSEAMLQLIPIFFQCRRHQCSVAMP
IEPDGIVVDATTHKWVYIARGVQPLVLDGTAFSEL

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTTCCGAACCTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

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FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGTCCTCCCACTTGACGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCACCTGGTGGCGACGCTGCTAGACCGTGCCTATGAGCCGCTGGGGCTGCAGTGGGGACTGCC
 CTCCTCGCCACCCACCAATGGCAGCCCACTTCTTTGAAGACTTCCAGGCTTTTTTGCCCA
 CACCGAATGGCGCCTATCTGACAAACAGGTACAGCCAACCATGTCACGTTCCGAATG
 GACACGTATGCTAAGAGCCAGCAGCTTATGTCAAGTTCCTGGAATGCTCTGATGACATGCT
 TATGACGATGGGACAGCGGCCACTGGGAGCGGCCAGATGCTCGGGCTTCCAGGAGC
 TGGTCTGGAACCTGCCAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTCTG
 AAGCAGCAGGCACGAGCACTCCATGGCCCTTGCTGCACTGGGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCCATGTGGGGCTGGGGCGCTGAGGGACACTCCCATCCCCGCTGGAACCTGTCCA
 GCGCGGACATATTACGCATGCGCTGGAAGCTGGTGCCCAACCATCACTTCGACCCCTGAG
 CTGGAAGCCAGCGCTTCCGAGACAATCTGGGTGAGGTTCCCTTGACACCCACCGAGGAGGC
 CTCACTGCCCTTAGCGAGTGACCAAGAGGCCAAAGTGAGACCCCAACCGAGTGTCTGCGAGG
 AGGACCAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGAGCGAGCAGAACTG
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGCGCCGAGTGCCAGCTGGTGAGCTAGTGGCGT
 GGTCCAGGGCTGCTGGAGGTCAACACAGAAATGTATATACTTACGATGCGCAGCACTGAGC
 GCGTGGAAACCGAGGAGGGCATCGGCTATGATTTCCGGCGCCACTGGCCAGCTGGCGTGAG
 GTCCACCTGGCGGCTTTCAACCTGCGCGCTTCAAGCACTTGAAGCTCTCTTTATCGATCAGGC
 CAACTACTTCTCAACTTCCCATCAAGGTGGGCGAGCAGCCAGTCTCACTTCTTAGCCAGA
 CTCGAGAGCCCGAGCTGGCCCCATCCACCCCATACCCAGGTACGGAACCAAGGTGATCTCG
 TGGCTCTGGCGCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCAGGAGAT
 GCTGCGTGCTCAGGCTTACCCAGAAATGGGTACAGCGTGAGATATCAACTCTCGAGTACT
 TGATCAACTCAACACATTGCGGGCGGACCTCAATGACCTGTCTGAGTACCTGTGTTC
 CCCTGGGTCTGACGAGTACGCTGTCCCAACCTTGGAGCTCAGCAACCCAGGCTCTTTCGG
 GGACTGTCTAAGGCTACCGGTGTGGTGAACCCCAAGCATGCGCAGCTCTGAGGGAGAAGT
 ATGAAAGCTTTGAGGACCCAGCAGGGACCATTGACAAGTTCACATATGGCACCTACTCTCC
 AATGACAGCAGGCGTGATGCACTACCTCATCCGCTGGAGCCCTCACTCCCTGACAGTCCA
 GCTGCAAAGTGCCGCTTTGACTGCTCCGACCGGCGAGTCCCATCTCGGTGGCGGCAGCCTGGC
 AGGCAGCCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGAATTCTTCTACTTTCTCT
 GACTTCTCTGGAGAACCAAGACCGTTTTGAACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTACCCCGTGCGGCGAGCTCTCTGAGGACTTCTACAGCAGCCAGCCG
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCAAGTCCCTGTGACGCTGTGAAGGAGCCACTCAACTCGGCTCTCA
 GCTGAGGAAGCAGCCCATCGCCTTGCACGCTGGACACTAATCACTAGGATCTTCCAGCA
 CCTGGACGAACCTCAAGGCATTCTTCGACAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAAGTCTCAGCAAGACCC
 ACCATGGGCGACCCCAAGACGACGCACTGCTGAGTGGCCGTGGGTGCCAGGCACTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCGGATGGAAGCTGCTATTACGCGGTGGCCACTGGG
 ATGGGCTGCGGGTGACCTACCCGCTGGCAAGCTGTTGAGCCAGCTGAGCGGCCAC
 CTTGATGTAGTAACCTGCTTGCACCTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCACTGGTGTGCTGGCGGCTCCTGCACTCAGGCTGGTGTGCTAGGCACTGTACGCG
 CAAAGCCTGTGCGAGTCTGTATGGGCACTGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT
 GAATGTACATGGTGTGTCTGATCTGAGGATGGAAGTGTGATCATACACACTGTACGCGC
 CGGACAGTTTGTAGCGGCATCTACGGCTCTGGGTGCCACATTCCTGGACCTATTTCCACC
 TACTTTGGGTCCGAAGCCAGATTGTGGTACAGAGCTCAGCGTGGAAGCTGCTGGGCTGGG
 CAGTCACTACTCTTGCACCTGTATTGATCAATGGAAGTGTGGGCTTCACTGCCCCCT
 GGCAGGACGCTCAGGCTGACGGGTGACAGGAGCTTTGTGTGCTGGGACCGGCCAGT
 GCGCCCTGCACATCTCCCACTAAACACACTGCTCCCGGCGCGCTCCTTCCGCTATGAAG
 GTGGCCATGGCGCAGCTGGCGCTGACCAAGGAGCGCAGCCAGTGTGCTGGGCTGGAGGA
 TGGAAGCTCATCTGCTGGTGGTGGCGGGGCAACCCCTTGAGGTGGGAGCGACCTGCGCG
 GGAAGCTGGGCGGTCTCGCGCGCATCTCCAGGCTGCTCTGGGAGAGCAGGAATACAAC
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGCTGCTCGGGCCCCCGCCCGGAGGCTG
 CGCGGGAGCCCGCCCGCAGAAGTCCGGCGGGAACACCCGGGTGGGACCGCCAGGCGGTGA
 GCGGGGCCCACTGCGCCAGCTCAGGATTTGGCGGGCGATGTTACCCCTCAGGATTTGGC
 GCGGAAGTCCCGCCCTGCGCGCTGAGGGGCGCCCTGAGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQAQTHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPOEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPPTLDLSNPAVFRDLSPKIGVVPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKELIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVLPWPASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDNTPSPISFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLISGSRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA
 WERPGAQVTYLSHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

CGGACGCGCTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAAATAAATACATCATGCAACCC
CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCAGGGGCTACTCAT
CCAAAGGCTAATCCAACGTTCTGTCTTCAATCTGCAAACTATGGGGTCTGGGGCTCTTC
TGGACCCCTTAACCTGGGTACTGGCCCTGGGGCAATGCGTCTCGCTGGAGCCTTTGCCTCCTT
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCTTGTGAG
ATAGCCCGGGTGCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGAGAACCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
TAAACCGCTATGCATACATCATGATCGCCATCTACGGGAAGAATAATTCTGTGTCTCAGCCAAA
AATGCGTAATGCTACTCATGCGAAACATTTGTCAGGGTGCTGCTCTGGACAAGTCACAGA
CTCCTGCTGTGTTCTTTGGGAAGCTGCTGGTGGTGGAGGCGTGGGGTCCCTGCTCTCTTTT
TTTTCTCCGGTTCGATCCCGGGGTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTATC
TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGTGGACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
GCTCCTTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCAGCTCCGGCCCTGATCCAGGACTGC
ACCCACACCCACCGTCCAGGCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
AAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCAGGCCTGTAATCCAACACTTTGAGAGGCTG
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGTGAAACCTCC
GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
TCGGGAGGCTGAGGCAGGAGAACTGCTTGAAACCGGGAGGCGAGAGTTGCAGTGAGCCGAGA
TCGGCCACTGACCTCCAACCTGGGTGACAGACTCTGTCTCCAAACAAAAACAACAACAA
AAAGATTTTATTAAGATATTTTGTTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCFVQGYSSKGLIQRSVFNLQIYGVLGLF
WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVVDKVTDLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMMSKSLLKILGKKK
EAPPDNKKRKK

000000.11001

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGTTTCGTGTCGGATTTCCGCAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTTC
 CAGTGTGACCAGCTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAAGCTTGAAACTGCT
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTCTGCAGCG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCCTGGTGCTCTACCAGCACTGGTCCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCTTTCGAGACATGGGTCTTCCCCGTAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGACAGCTTTTACGATTCATTTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAATCGCCAAGAAGCAGCTGCGAGGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTCTAGCCGGCATCCCTAAGCCTGCTCAGCAAACCTGCTCA
 AGTCTTTGTGTGTTGCAAAAGAACCGGCGTGCAAACTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCAQAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCTTAGGAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTCATTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDDEHSGNDS DGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH
VSRHNRHNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGFFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTTVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNF DL SVIELKAEDRSKFL
DALISLLS

000027.11901

FIGURE 28

GTACCTCAGCGCAGCGCCAGGCGTCCGGCCCGGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

0999279.11901

CAGGAAACCCTCTCTTTTGGCTGTGGATTGGGACCCCTTTCCAGTACCATTTTTCTAGTGAAAC
 CACGAGGGCAGCATACCGAAACACCCCTCACCCAAAGGAATAAGCATACAGCCCAAGTTGG
 GCTGACTTTTGGCTATAGAAAAGAAAGGAAGCAAAAAGACAGCACTTTTGTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAGAAAGACCCCTCTCTGAGCTATTTTACAGCTTTTAAACATT
 GAGTAAAGTAGCCTCCGGTCACCCATGGCTGACAGCGCCCTGGGTCCCGCTCTGGGACGCGCTC
 CTGCTCTCTCTGATGTGTGAGATCTGATATGTGTGGAGCTACCTTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGCTGTGTGACTCTGAGTAACCCCTGGATCTTGCCCATGTATCTCAG
 CCTCTCTCTCCGGCGCCCGCCACGCCCTGCTTGAGATCAGACCCATCAATTATATACCAATT
 CTGAAGGGGTGACAAAAGGGGACCCAGAGCCCAATGGGCGCTCGACGGGTACATGGCGAGGGGG
 TCCCCAAAGGGGAGCCCTGGCCCTCAGGGCAGCAAGGGGTGACAAAGGGGAGATGGGACAGCCCG
 GCGCCCGGTGCCAGAGCGCTTCTTGCCCTTCTCAGGTGGGCGCAAGACGCCCTCTGCACAGC
 GGCAGGAGCTTTCAGACGCTGCTCTCTCTGAAGAGGGTCTTTGTGAACCTTGAATGGGTGCTTTGA
 CATGGCGACCGGCGAGTTTGTCTGCTCCCTGAGTGTGGCATCTCTTTCAGCTCTCAATGGTGC
 ACAGCTGTGGAATACAGGAGAGCTAGCTGCACATTATGTCATAACCAAGAAAGGCTGTGATCT
 CTGTACGCGACGCCAGCGAGCGAGCTAGCATGCAGAGCCAGAGTGTATGCTGGACCTGGC
 CTACGGGACCGCGTCTGGGTGGCGCTCTTCAACGCGCAGCGCGAGACGCCATCTACAGCAT
 ACAGCATCTGCACCTCATACCTTTCAGCGGCCACCTCATCAAGGCGGAGGACGACATGAGGGG
 CTTCTGGGCGGCGCTCCCGGCTGGAGAGCTCAGGTGTGGTCCGCTCCGCTTCGAGGGGCTCAG
 TTTGACCTGCTGTGAAGCAGGAAGCCCGAGGAGGTCCCGGGGAGCTGGCATCTGGGGAAGT
 TGGCTCTTCTATCTTGCTGCTCATCTCCCGAGCTATTTCTGCTCTCTCTCTCTCTCTCT
 TCCGACTATTTTAAAGAGCTTGCTAACCTAAATATTCTAGAATTTCCCGAGGCTCGTAGGCC
 AGCACTTCTCAAATCTGGAAATGTCATGCAATCACCCGGGGTTCGTGTAAATGCAATTTCT
 GACTCAGCAGCTCTGATGGGTTCAGGAATCTGTGTTCTCATATGTCTCGGGTAGTGTCTG
 ATGGGCTCAGTCTATGAACACCACTGGAGCAACAGGTTCTAGAGACTTTCTCAATATTCTAT
 TACTTTTTCGAACATTCTGGAATCTCTCCCAATCTAGAATTCTCCCAACATTTTTTTTCT
 TGAGACAGAGTCTTGCTCTCTGTGCCAGGCTAGAGTGCAGTGGTGCAGATCTCAGTTCAGTGC
 AACTCTGCCCGCGGGTGAAGGATCTGAGCGAGCTCCCTAGTGGTCCGGATTTAC
 GTGGCTCTAGCAAGCTCTGATTTTGTATTTTGTAGTAGAGTAGGGTCTACCAATA
 CTGGGGATTCAGTGTGACGACCATGAGTCTGAGGTCAGCCGCTGGCTCTCTTCTTAA
 CCTCTCCGGCTCCCGCTCTATGTTCTCTTTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT
 TGACACACTGCAGCCACGCTTATTATTATCTTAAACATGTAGCACTACCTCTGCTCT
 GGGTCCGGGGAAGGGTAGGGGTGACAGCAGGCGCTGCCCTGCCCTCAGTGACTGTGCGC
 CTCAGCCAGCGCGGGGAGGATGTGTACATAGGTTTAAAGCAGCCAGTACGTATGGG
 GCGGTGTTTCTGGGTGTTTCAGGTGCTGCTGTGCTCTCAATACCAACTGCTCCCAAGGCTGG
 TCCGAGCGGGGTCCCGGTGCGCAGGGCGAGGTATCTCTTCCCGTTCTCATCCACCTGCCAG
 TGCTCATGTTTACAGCAAAACCCCAAGGGGCTGGCCAGCTCAAGGTTCTGTGAGGAGAGG
 ACCAGGAGTTTGGGGGCTTTGGGGGGTGAAGTGGCCCGCAAGATGGAACCAACACCA
 TAGCTCTCCCCACAGCTCATACGGCATCTGCGAGAAGACTGCCCTCTCTCACTGGATCCC
 CTCTCGCTCTCTCCAGGGGCTGTCCAGGGCGCTTGCTCAGTCCCTTACCAAACTCATCT
 GAACTTCGGTTTCCCCAGGGGCTCAGCTGCCCTCAGACATCATGTCTGTGCCAGGTGCT
 CTCTGCCCTCATGCCCTCTCACGGCCAGTCCCCAGCTCTCAGGCTTTTATCAAGTGT
 CTAAAGGCGGGGTGGGACGCTCTGCTCTCAGAGCCCTCTCCGGCTGGTGTGCTCTTAC
 AAACACCTGCAGGAGAAGGGCCCGAAGGCCAGGCTTTAGAGCCTCAGCAGGTCTGGGG
 AGCTAGGACAAAGGAGGACCTCAGGCCCTTCGGTTTCTTCTTCCAGGTTGGGTTGGCTGGT
 GTTCCCTAGGCTTTCAAACCCAGGCTGGCTGCCCTTCTCCCAAGGAGGAGCGGCTCCGC
 CCAATTGGTGTCTAGCTAGACTCTGGGGCTGAGGTGCCCGGGGGGTGACTCTGTGTCTCAG
 AGCGGAGGAGCGGTGGCTCATGTGGCCAGTAGTGGAAACAGGCTGTACAACTGTCCAGGA
 AGACTGTGCTATAAACACCTGCTGCTGATCTCTGCCCTGCCCTGACCCCGCAGCGGCTGCC
 GTCCAGCATGTTATAAGAACTGCTGCTCTCTCTTGGAAAAAATAAAAAA

FIGURE 30

MVTAALGPVWAALLLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITLLKGDKGDPGMPGLPGYMGREGPQGEFPGPGSKGDKGEMGSPGAPCQKR
FAFSVGRKTALHSGEDFQTLLEFVFNVLGCGFDMATGQFAAPLRGIYFFSLNVHWSWNYKET
YVHIMHNQKEAVILYAQPSERSIMQSGVMULDLAYGDRVWVRLFKQRQENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGCCCTGCCCGCCCGGCTCCTGCGCGCGCCGCCCTCCCGGGACAGAAAGATG
 CTCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGG
 ACCACGGTGCCTCCGAGACGTGCCACCCGACACGGTGGGGTGTACGCTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGAGCTTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTGAC
 AGAACCGATCGCCAGCCTGCCAGCGGGTCTTCCAGCCACTGCCAACCTCAGCAACCTG
 GACCTGACGGCCAACAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCTGCGGCGCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACG
 TCGACCGCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGCGGGCTGCAGCAGCTGGAC
 AGGGGCTCTTACGCGCTTTGCGCAACCTCCAGCAGCTGGATGTGTCGACACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCGCTCCGGGGCTGCAGCGCTGCGGCTGGCCGGCAACAC
 CCGCATGGCCAGCTGCGGCGCCGAGGACCTGGCCGGCTGGCTGCCCTGCAGGACTGGATG
 TGAGCAACCTAAGCTGTGAGGCGCTGCTTGGCAGCTCTCGGGCTCTTCCCCGCTGCGG
 CTGTGCGGAGCTGCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCTG
 GGTGCGCGAGAGCCAGCTCACACTGGCAGCCCTGAGGAGACGCGCTGCCACTTCCGCCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCAGCCAC
 ACCACAGCCACAGTGCCACCACAGGCGCTGGTGCGGGAGCCCAAGCCTTGTCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCCGCTTCCA
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTTGCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACCTTGGCGTGTGTCGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA
 CGCCGAGGCCACACAGGTCCCTGACCTGGGCATCGAGCGGTGAGCGCCCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACAGGTCACCCAGCTGCGGCCCCAACGCCACTTACTCCGTCTGTGTCATGCCCTTGGGG
 CCGGGGCGGTGCCGAGGGCGAGGAGGCTGCGGGGAGGCCCATACCCCCAGCCCTTCCA
 CTCCAACCCAGCCAGTCAACCCAGGCCCGGAGGGCAACCTGCCCTCTCTATTGCGCCCC
 CCTTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGCGG
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCT
 GGAAGTGGAGGAGTGAAGGTCCCTTTGGAGCCAGGCCGAGGCAACAGAGGGCGGTGGAG
 AGGCCCTGCCAGCGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCTGGCCCTC
 CAGTCACCCCTCCACGCAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCGG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCTCCTGCTGCCACACAGCTAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGAGACAGGGCTGTGTGACCACAGCTGGGGCTGTTCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCCATGAGGACAGTGTGCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGACGGCG
 GGCCTTGCCATGTGCTGTTAACGATGCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA
 CCCTGGGGCCAGTGAAGGAAGCTCCCGGAAGAGCAGAGGGAGAGCGGTAGGCGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCATTTATTCTG
 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGAAGACAACAGATGATAG
 AAGGCTTTTTGTAAGAAAAATAAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPDPDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNEIRALPPLRLPRLLLLDLSHNSLLALEP
GILD TANVEALRLAGLGLQQLDEGLFSRLRLNLDLDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG
PWVRESHVTLASPEETRCHFPKKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPPTAPPTVGVPVQPDCCPSTCLNGGTCHLGRHHLACLCPE
GFTGLYCESQMGQGTTPSPTPVTPRPPRSLTLGIEPVSPSTLRVGLQRYLQGSSVQLRSLRL
TYRNLSGPDKRLVTLRLPASLAETVTQLRPNATYSVCMPLGPRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGAAYCVRGRAMAAAAQDKGQVGPAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

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FIGURE 33

GAATCATCCACGACCTGCAGCTCTGCTGAGAGAGTGCAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCTTCATATGAGGAAATAAGTGGTAAAAATCCTTGGAAATACAA**ATG**AGACTCATCAG
 AAACATTTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTATGCTCCAGAGCTGGCAG
 AAGAAGAGGGAATGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCGAGCCCAACAGCACCTGGATTTATCCTATAACCTCCTTTTCAACTCCAGGTTCCAGA
 TTTTCTATCTGTCTCAAACTGAGAGTTTGTATCTATGCCATTAACGAATTCACAGCTGG
 ATCTCAAAACCTTTGAATTTCAACAAGGACTTAAGATATTTAGATTGTCTATAACAGCTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGCTCAGGTATTTAGATCTTCTTTTAAATGACTT
 TGACACCATGCTTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTGA
 GTGGGGCAAAAAACAAAAATCAGATTCCAGAAAATTGTCTATCTGCATCTAAATCTGTCT
 TTCTTAGGATTTCAGAACTCTTCTCTATTATGAAGAAGGTAGCCTGCCATCTTAAACACAAC
 AAAACTGCACATTTGTTTTACCAATGGACACAATTTCTGGGTTCTTTTGGCTTGTGGAATCA
 AGACTTCAAAAATATTAGAAATGACAATATAGATGGCAAAAGCCAAATTTGAAGTTATGAA
 ATGCAACGAAATCTTAGTTTAGAAAAATGCTAAGACATCGGTTCTATTGCTTAATAAGTTGA
 TTTACTCTGGGACGACTTTTCTTATCTTACAATTTGTTGGCATACTCAGTGGGAACACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTGTACTAC
 TCAAATACTGTAATGAGAACATAAAAAATGGAGCACTGTACATTTCAGAGTGTTTTACATCA
 ACAGGATAAAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAAAT
 CACAATGCCCACACATGCTTTTCCCGAATTATCTTACGAAATTCAAATTTAAATTTTGGC
 AATAATATCTTAAACAGACGAGTTGTTTAAAGAACATCCAATCGCTCAGTTGAAAATCTCT
 CATTTTGAATGGCAATAAACTGGAGACACTTTCTTAGTAAGTTGGCTTGTGTAACACACAC
 CTTTGGAACTCTGGATCTGAGTCAAAATCTATTACAACATAAAATGTATGAAAATTTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTACATAAATTTGTCTGATTCTGTCTCAG
 GTGCTTGCCCAAAAGTATTCAAATACTTGACCTAAATAAACAACCAATCAAACCTGTACCTA
 AAGAGACTATTCATCTGATGGCCTTACGAGAACTAAATATTGGCAATTTTCTAACTTCTG
 CTCCTTGGATCAGTCATTTTCAGTAGACTTTCAGTTCTGAACATTTGAATGAATCTTACTTCT
 CAGCCATCTCTGGATTTTGTTTCAGAGCTGCCAGGAAGTTAAAACTCAAAATGCCGGAAGAA
 ATCCATTTCCGGTGTACCTGTGAATTA AAAAATTTTATTTCAGCTTGAACATATTCAGAGGTC
 ATGATGGTTGGATGGTCAGAGCTTATACACCTGTGAATACCCCTTAAACCTTAAGGGAACATAG
 GTTAAAGACGTTTCACTCTCCACGAATTTATCTTGAACACAGCTCTGTTGATTGTACCAATTT
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCCTTCTGCTGTCTCCACTTGTATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACAAACATGGCAGAGGTTAGGAAAACAACCCA
 AGAACAACTCAAGAGAAATGTCCGATTCCACGCAATTTATTTCAACAGTGAACATGATTCTC
 TGTGGGTGAAGAATGAATTTGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTTCG
 CTTTATGAAAGCTACTTTGACCTGGCAAAAGCATTAGTGAAATATTGTAAGCTTCATTGA
 GAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCACTTTGTCCAGAAATGAGTGGTGGCATT
 ATGAATTTCTACTTTTGGCCACCACAATCTCTCCATGAAAATCTTGATCATATAATCTTTATC
 TTACTGGAACCCATTCCATTTCTATTGCAATCCCACAGGTATCATAACTGAAAGCTCTCTCT
 GGA AAAAAGCATACTTTGGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCA
 ACCTTCCAGCTGTATTAATGTTAATGTATTAGGCCACAGAGAAATGTATGAATGCGAGACA
 TTCAACAGATTTGAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGTCT
ATAAAATCCCACAGTCCTTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATA
 CAACCTTTATGATGGCAATTTGACAATATTTATTAATAAATAAGGATGTTATCCCTTCATA
 TCAGTTTCTAGAAGGATTTCATAAGAATGTATCCTATAGAAAACCTTTCAAGATTTTATAAGG
 GCTTATGGAAAAAGTGTCTCATCCAGGATTGTTTATAATATGTAATGTAATATAATATTA
 AGTGGCTCACCTCTGTAATCCCAGCAATTTGGGAGGCCAAGTGGGTGACCCAGCAGAGGTCAA
 GAGATGGAGAGAGTGGGCAACATGGTGAAACCTGTCTCTACTAAAAATGTGGCCAGGTGC
 GCTGGGCGTGTGGTGCAGCCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCAGGAGGAATCG
 CTTGAACCCGGGAGGTGGCAGTTGCACTGAGCTGAGATCGAGCACTGCACCTCAGCTCGGT
 GACAGAGCGGAGCTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAATATTA
 TCAATGGCCCAAAAAATAAGTCTAATTCATAAAATATAGTACATATGTAATATAATATTA
 CATGCCACTAAAAAGAAATAGGTAGCTGTATATTTCTGGTATGGAAAAACATATTAATAT
 GTTATAAATCTTAGGTTGGTGCAAACTAATTTGGTTTGGCCATGAAATGGCATTTGAA
 ATAAAAAGTTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGCTGGGAGGTTGGA
 TTACAGGGAGCATTTGATTCTATGTTGTGATTCTATAATGTTTGAATTTTAGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

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MRLIRNIYIFCSIVMIAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHVSVKLRVLILCHNRIQQDLKTEFENKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPMPCIEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTPHYEESLP
ILNTTKLHIVLPMDFNTFWVLLRDLGDKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVLDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLITISNAQPMHMLFPNYPFKFYQLNFANNILDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENCSPWETVVMNLSYNKLS
DSVFRCLPKSIQIIDLNNNQIQTPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLEYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHLSCNTALLIVTIVIMLVGLGAVAFCCFLHFDLPWYLRMLGQCTQTWHRV
RKTQTQQLKRNVRFAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKISFVLSPNFVQNEWCHYEFYFAHNLPHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

GGGGGGCTTTTGGGGCTTTGGCTGCTTGGAAACACTGCGCTCCAGAGACCGGCTCGAGGAGTGGTGGGGGAAAGG
GAGGAGGAGGAGGAGGCGGGGGCGGCCCTCGCGCGCGCCGGCGCTTCGCGCGCCCTTCGTCGCCCGCCG
CCAGCCACGACCGCCCTCGCGGGCGGCTACACGCGACGACGCGCGCCCTCGCGGCCACGAGCGCGCGCT
CTGCTGTGCGCTTCGCGCTTCGCGCGCGCGGCTTCGCGCGCGACGCGCGCGCGCGCGCGCTGACCTGAC
CCTCGCGCTTGGGCGCGGGGCGGAGCAGCGATGTCGCGCCCGGGGACCGCTACCCAGCGCTGGCCCTTGCTCT
CTGGCAGTACCGCTTGGCGGGTCCGAGCGCCAGGCGCGGACGCGCTCGAGGACCGCTGATTATTCAGGCGAGGAT
CTGGAGCGGGGAGCTTACTACGCGCGCGCGCGCGCGCTTCGAGAGCTTCTCTCGCGCTGCTGCGGGGCG
CGGGGAGGAGTGGAGGAGCGCGCGCGCGGAGCGCGGCGCCCGAAGAGGGCACCGAGCCCAAGAAAGCTCCG
AAGGAGGAGAGTGGCTCGGAGCGCTCCACAGGCTAAACACGACGACAAAAGATTTATGAGACCAAGAG
CTCTGAGAGAGTGCACAGGATGATCACAGTGTCCGTGTGGCCCTGGAAGATGTTCAGAGAGAGTTGCCCATCT
TGTGTCGGAAACCTTAAATACAGACTTCAGCTCATGAGTCCACGGTGAAGCGATTGCTTGGCTGGGGGCA
CTCAGGGAGAGACTCAACATCCAGCGGGGCAATTAATGAAAGTATTATTAATCAGGAGCGTGTGGCGGGGAAG
AATATGACTCTCAGAGTGGATTGAAGTGATGTCGAGGCTGACGACGATTAATGGTGTATCATCAGGGA
GGAATCTCCCTTCGTGAGTGATCTGGGTGATCATCTTAAGGTGATGTGTGAGCAATGACAGCCACGCTGGGTG
ACTGTTAAGATGGATGGAGACATGATTGAGGAAACAGTGAAGAAGATTCCTGTTCTCAATGAGCT
ACCCGTCGCCATGTGGCGCTCATCCGCAATAACCTCAGTCTGGTTTATATGGAGACATTCGATGATGA
GATGAGAGTCTGGGCTGCCACTGCGACATCTAATTAATTTATPACCGCGGAACGAGATGACCAACT
GATGACCTGGATTTAAGCACCAATATAAAGGAATGCGCAGTTGATGAAATGTTGAATGAATGTGTCC
CATATACCAAGAAATTTACAACATGGAAAGAACCGAGCGCTGAAGCTGTATGCTGTGAGATCTCAGATC
ACCTCGGGGAGCAATGAAGTCGCTGAGCCGAGTTCACATACATCGCGGGGCGCCGCGCAATGAGTGTGTGGC
CGGGAGCTCTGTGTCGTGGTGGCATGTTGCTGTGAGGAGTATGGCGCGGAAGTCGCGCATCTGTCACCT
GTGGAGGAGAGCGCGGATTCAGCTCTCCCTCCCTCAACCCGATGACATGACAGAGGCGTACAGAAAGGCTC
CGAGCTGGAGGCGTGTCTCTGGGCGCTGGACCCAGTGGAAATGGCATCAAGAACAACTTTCTGATTTA
AACACGCTCTCTGGGAGGAGGAGGATGAGAGATGTCGCCAGGAAAGTTCCCATAGATTTGCAATCCCT
TGAGTGGTTTCTGCGAAAGTTCACGGTGGTCGCGAGACGAGACGATGATAGCTCTGATGGAAAGAAATC
TTTTGTGCTGGGCGCAACTCTCAGGGCGCGCAGCTGTGCTGGCGTATCCTAGACACTGTTGGCGGCTCCCC
TGAAGAGCGAGGAACACCCCCACCCGATGACACTGTCTCCGCTGGTGGCTACTCTATGCTGCAC
ACACGCGCTCATGACAGACGCGCGGAGGAGGCTGCCACAGTGGAGGACTTCAGAGAGGAGGAGGCACTGTCA
ATGGGCGCTCTGCCACACGCTCGTGAAGTGTGAAGAGTTTCACTACTCTACATACAACTGTTCTGAAGTCT
TCATCTACGTTGGGCTGATAAATACCACTGAGAGCGAGCTCGCGGAGGATGGGAGAAATACCGGGAATCT
TCTGATGGTGTTCATGAGCAGGTTTCACTGTGCATTAAGGCTTGTGAGAGATTCACATGGAAAGAAATCC
CAAAAGCCCAATATCTCGTGAAGGCAATTAACCATGATCTCGAACAGCAAGTGGGAGTTACTGGCGGCTCT
TGAAACGCTGGAGAGTATGTGTCACAGAAAGCGCGAAGTTTCACTGATCCACAGAAACTGTATGGTGG
CTATGACATGGGGGCGCAAGGTGTGACTTCACACTAGCAAAACCAACATGGCGAGGATCCGAGAGATCATGG
AGAGTGTGGGAAGCGCCGCTCAGCTGCGGACGAGGCGGCTGAAGCTCGGGGGCGGAAGAGACGACGCG
GCGTGCACCTCTGGGCCCTTGAGACTGCTTGGGACCACTGCAAAATTAACCAACTGTTGATAGCTCCATG
TGCACTCACTCACTGTTGTTTCTCTGTATTAAGAAGTCTGGAGAGAGGCTGTCATTGAGGCGAGCTCC
CAAAAGGAGGCTGGAGGCTGAGGCTGTTTCTTCTTCTGTTCCCAATCTCTCAAAATTAACCTTGGACAGCA
CGAGAGAAAGCTGATGGAGTGAAGAGACTCAGCAGAGCCATCTGGGAATCAGAGAGGAGAGGAGGAGG
GAGCTGTCCGTCGATGAGCTCTGCTGCTACATAAAGAGAGATTGTGTTGTTCTCCCTGTTTGGCTGGACGAGG
GTCCACGCTCAAGTTTGAACATTGCACGATAAATTCGACATTTCCCGAGCTGGGCTGCCCCAATGTATCCA
TTTGAGATGCTCCAGGCGCTTAAGAAATCCACCTCTCTGGCGCTGGGACGTGCAAGCTGCTCAAAATTA
ATTCTGTGTTCTTTTGACATAGCTCATTGCCAAAGTGCACTCAGTGAAGCTTTGAACTTTTGTAGTCTCT
TTTTCACAAAGGAGTGTCTGCAAAAGGAGAGGAGGCTGAGATCACTCAGGAGTTGTGTGGGCGACAGCA
TGAGCTCTTCTTGCACAAATTTGGGTCATAAAGACACCCCAAGTCCCTGCTGATTCAGTGAAGTCTGGAGT
CCCCGCTGAGGAGGAGCGAGGTCGACCTGCTCTGAAGGCGCAGAAATTTAGCTGTGATCTCTCTTTTAC
CTGCTAGACTGGAAAGAGCGAGGATGGGGTGGCTTGAAGGCCCTCTCTGCTGAGTATGGCCCTGTGTG
GAATTGAGTGTCTATGGTTGGCCCTCATATCAGCTGGGAATTTATTTTGATTTGATAGTGAAGTCCGATCTCCA
GATTAGGCTTAATGATTAAGAAACTCTTAGATTTATCTGTGAGCATGATTTGGGAAGATTTGTAATTTA
CTTGCAAGAAATAGTATGCTCTCACTTTTGTATTTGTCTGCTCACTGACCTGGGAAAAATGAAAAAATAA
AATAAAGCAAAATGTAAGCCCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPHYARPEPELETFSPLPL
AGPGEEWERRPQEP RP PKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGLRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLRTFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWTVKNGSGDMIF
EGNSEKEI PVLNLPVPMVARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCNITRIYINIGKSHQGLKLYAVEISDHGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGI DINNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAMWEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEVVWNTAKESLIVFMEQVHRIGKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLL
NPGEYENNAKAEFGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRGKRROG

FIGURE 37

CTAAGAGGACAAAGATGAGGCCCGGCCCTCTCATTCTCTAGCCCTTCTGTTCCTTCCTGGCCAAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCCGACGCTTAGGCAGCGGAGGTTCTGTGTCGCCAGTTGGT
 TTCCAATTTCACCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTCCTTCGCCAGACACCACCTTTTC
 CCGTGGACAGATGGAACCGTTGGAATTACAGCTCATGTTCTTCTCAGAAGTTTGAGAAAGACTTTCTCAA
 GTGAGGGAATATGTCCAATTAAATTAGTGTGTATGAAAGAAACTGTTAAACCTTAACCTGTCGGAATTGACATCAT
 GGAAGAGGATACCAATTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAGAAC
 TGGTCATACAGCTGAAGGAGAGTTTTGGTGGAAAGCTCAGAAATTTGTGACCAAGCTGGAGGTGGAGATAAGAAAT
 ATGACTCTCTTGGTAGAGAGCCTTGAGACACTAGACAAAAACAATGTCCTTGCCATTTCGCCGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAAACACCCCTGTGCTGCCACCTCTCCCACTC
 CAGGGAGCTGTGGTCATGTGGTGTGGTGAAACATCAGCAACCGCTCTGTGGTTCAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCAAGCATCCAACAAGGACTGTATTGGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGCTCAAC
 ATGTACAACACCGGAATATTGCCAGAGTTAACTGACCAACAACAGATTTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCATAATAACCGCTTTTCTATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTATTATTATCACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACACTT
 CAGGTGCTAAACACTTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCTTCATGGTATGTGGGGTTCT
 GTATGCCACCCGACTATGAACACCAGAAGAGAGATTTTTTACTATTATGACACAACACAGGGGAAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGACAGACATTAACTATAAACCCTTTTGACAGAAA
 CTTTATGTCTATACGATGTTTACCTCTGAATTATGATCTTTCTGCTTTCGAGAAGCCCCAGTAAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAAAAATGTTTGTGAAAAAATAGTCTTCCACTTACTTAGATATCTCGAGGGGTGT
 CTAAAAGTGTCTCATTTTGACGCAATGTTAGGTGCTAGTCTTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGCTGAGTTCTCTTGGGAATCATCTGCCCTTCAGGCGCATTTTGTCAATAAAGCTGTCTTAGGGTGGGA
 TTGTGAGAGGTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTCTCACTAGAAGCCTTAAATTA
 GGAATTAAGGAACCTAAAACTCAGTATGGCGCTAGGGATTCTTGTACAGGAAATATTGCCAATGACTAGTC
 CTCATCCATGTAGACCACCAATATCTCCATGCCGTGGAGAAGCTGGGCACTTAGTATAGGTAGATTATATCTC
 GGAGCTCCTCGAGGGACCAAATCTCCAATTTTTTTTCCCTCACTAGCACTGGAAATGATCGTTTGTATGGG
 CAGATAAGTAAATTTGGCATGCTATATATCTACATCTGTAAGTGCTGAGTTTATGGAGAGAGGCTTTT
 ATGCTATAAATTGTCAATGGCAATTAATCCAGAGGATCTGTAGATGAGGCACCTGCTTTTCTTCTCTC
 ATTGTCACCTTACTAAAAGTCAGTAGAATCTTCACTCATAACTTCCTTCCAAGGCAGCTCAGAAGATTAG
 AACCAAGCTTACTAACCAATTCCACCCTCCACCAACCCCTCTACTGCCACTTTAAAAAATTAATAGTTTT
 CTATGGAATGATCAAGATTAGAAAAATTAATTTTCTTTAAATTCATTAGGACTTTTATTTACATGACTCTA
 AGACTATAAGAAATCTGATGGCAGTGACAAAGTGCTAGCATTTATGTTATCTAATAAAGACCTGGAGCATA
 TGTGCAACTTATGAGTGTATCAGTTGTTGCAATGTAATTTTGCCTTTGTTTAAAGCTGGAACTGTAAAGAAAT
 GAAAAATTAATTTTTTTTCTAGGACGAGCTATGAAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGATT
 TGGAAACCTCTGCGGTGATGTGATGTGCTCTGTGCTTTGAATGACTTTTATCATCTAGCTCTTTGTGCTATT
 TCCTTGATGTCAAGTCTCAGTCTATAGGATGGCAGTTTAAATGCTTTACTCCCCCTTTAAAAATAAATGAT
 TAAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 38

MRPGLSFLALLFFLQQAAGDLGDVGPPIPSPGFSSFPGVDSSSSSFSSSSSRGSSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVNVISKPSVVQLNWRGFSYLYGAWGRDYSPQHHPKGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYGQSGTAVYNNNMVNMNTGNIARVNLTNTIAVTQTLPNAAYNRR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGVLYATRTMNRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

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FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGNGGCCCATGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCCGAGAAAGAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTTGTGACGTTTGTGGAGATGTTGGGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCTAGTTTGTGTGGAGTGCCTCGTGTGTGCTATGCCGATGCTGTCTGCTATGGAAAC
 AACTCCACTGTTAACTAGATTGATCTATGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGT
 TGTAAATGTTGATACCAAGGAATGGAAGAACAACCTGAATAAGATTCTCTGGATTTGTGAGAAATG
 AGAAGGTTGTGTCCCTTGTAACTATTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTGT
 GGTTTGGCTATGTTCTATCTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGCACAAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTTGCAATTA
 TTATTGGGTCATTTCTTCAATCCAGAAGGAACTTTACAACCTGTGTGGTTTTATGTAGGCATG
 GCAGGTGCCTTTTGTTCATCCTCATACAACCTAGTCTTACTTATTTGATTTTGCACATTTTGT
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACTCGAGATGTTGGTATGCACGCTTGT
 TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTGTCTTGTGTCTAC
 TACACTCATCCAGCAGTTGTTTTCAGAAACAAGGCGTTTATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAATCAACAACCAAGATCTGGTT
 TGTTACAGTCTTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
 GAACCAGAAACAAATTGCAACCCAAGTCTACTAAGCATTAATTTGGCTACAATACAACAAGCAC
 TGTCCCAAGGAAGGGCAGTCCAGTCCAGTGGTGGCATGCTCAAGGAATTTATAGGCTAATTC
 CTCTTTTGTGTGTGTATTTATTTCCAGCATCCGTTACTTCAAACAATAGTCAGGTTAATAAAA
 CTGACTCTAACCAAGTGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTATGGATC
 ACTGGAGGATGGGGACGATGTTTCCCGAGCTGTAGATAATGAAGGGATGGTGTCACTTACA
 GTTATTCCTTCTTCTTCACTGCTTTTCTGGCTTCACTTTATATCATGATGACCTTACC
 AACTGGTCCAGTATGAACCTCTCGTGAGATGAAAGTCAAGTGGACAGTCTGTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATCGTGTGTATGTTTGGACACTCGTGGCACCCTTTGTTCT
 TTAACAATCGTGATTTTGAAGTGAAGTGTGAGACTTCTAGCATGAAAGTCCCACTTTGTATTATTC
 TTATTTGAAAACAGTATTCCTCACTTTTGTAAAGTTGTGTATGTTTGTCTCCCATGTAAC
 TTCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTTGTCAATTTTGTATTTTTCTTACCAA
 GTGCATTTGATATGTGAAGTGAATGAATTGCAAGGAAAGTTTTATGAATATGGTGATGAGT
 TAGTAAAAAGTGCCCATTTATTTGGGCTTATTTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACAAAATTTGTTTGTATTTTAAATTTATATAGACCTTAAAGCTGTTTGTAGCAAGCATTA
 GCAATGTAAGGCTGCCTTTTGAATATTTGATGTGTGCTGGCAGGATAGTCAAAAGAAC
 ATGTTTATTTTAAATTTATAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTATTAGTGGCAATAGTGTAGG
 TTATGGATGGAGGTGTGCGTACTTAAATTTGAATAACAGAGTAAATGATCTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAAGTGTGTTTGGTTGTTTTAACTCATGAAGTATGGGTTGAGT
 GGAATGTTTGAAGTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA
 AGGAAGTGTGTTGAAGTCACTTTGAAAGTTAGTTTTGGGCCAGCAGCGTAGCTCACCTTT
 GGTAAATCCAGCACTTTGGGAGCTTAAAGTGGGTAGATTACTTTGAGCCAGGAATTCAGACCA
 GCTTGGCACATGGTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCTGTGGTC
 CAGACTCAGAGGCTAGTGAAGATTGCTGAGCCAGAGCAAAAGTTGCACTGAGCAAGTCA
 CGTCACTGCACCTAGCTGGCAGAGTAAGCCAAAAAATATATATATTTGAAATCAAGG
 AGGCAAAAATTTGACAGGGAAGGAAGTAACCTGCAAAACCACTAGGCTTTAGTAGGTACTTAT
 ATAAAACTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA
 GCTCAGATAGCTAATTAGGAATTTCAAGTTGGCCAATAATAGCATTTCTCTGACATTTAA
 AAATAATTTCTATCAAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT
 GATGTGAATGCTGTGTGTCAGCATGACCCATAACAGGTGAGAAGATGATGGAATGTTTT
 AGAATAAATCCTGCTTATAGTATACTACAGATTCAAAAGATGTTTAAAAATGCTTTTGTAT
 TTACTGCCATGTAAATGAAATATATAGATTATTTGTAACCTTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTTATGTTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAAAATCTCAAAAT
 TCTTTGTTTTAAAAATTTTATTAATGTGAATGGAATATAAATCAATTTCACTTAAATCCCCAAC
 TTATTTCTGTGTGTAGACATTTGATTCACAATTTTGAATGGCTGTGTTTTACCTCTAAATTA
 ATGAATTCAGAGAAAAA

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FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGWPCNILVGYKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMylTWSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVITYSYFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

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FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAAC TTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNTATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCAC TTTTNTTGCTTGTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAAC TGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCATNTTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTT TTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAAGTATGATCTATGCACTT
TTCTTGCTTGTGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGAAGAACAAC
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 45

GCTGTCCTTAGTGAAACAANTCCAACCTGTAACTGGATTGATCTATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTCCCAGGATTGGANGAACAACTGAATA
AGATTCCGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACCTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

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FIGURE 46

CTCGGGCGCGCAGGAGCTCGGTTTGGCCCTGCGATTGAGCTGCGGGTTCGCGGCGCGGCGCGGCTCTCCAAT
 GGCATAATGTGTGGTGGAGCGAGCGGAGGCTTTCGGCAAGGCGAGTCGAGTGTTCGAGACCGGGGCGAG
 TCCTGTGAAAGCAGATATAAGAAAAACATTTATTAACGTGTCTATTACAGGGGAGCGCCGCGCGGGCTGTGCGC
 ACTCCGCGCGGCAACTTTGGCTTCCTCCAGCTCCGAGAGAGGAGAAAGCGAAAGCGAGAGTCAC
 GTGTTTTCAGCCAACTGGACCTCATGATGGCCCTCTGTAATTTATCAGATATTTGATTTATTACGATGCC
 CCTCGTTGTGTGTAGCAGACACACAGTGCACAAAGGCTCTGGCTCGCTTCCTTCCTCGTTTCAGCTTC
 TGGGCGAATCCACACTCTGTTTCAACTCTCCGCGAGGGCGAGGAGGCGAGAGTGTGTGCAATCTGCGAGTG
 AAGAGGCGAGGAGGAAAAAAGAAACAAAGCCACAGACGCAACTTGAAGCTCCGCGATCCCAAAAGAACGACGAT
 CAGCAAAAAAAGAAAGATGGGCCCCCGAGCCTCGTGCTGTGCTTGTCTCCGCACTGTGTTCTCCCTGCTGGG
 TGGAGCTCGGCTCTCTGTGCGCACACCGCCTGAAAGGCGAGTTTCAGAGGACCGCAGGAACATCGCCCA
 ACATCATCTCGTGTGCTGACGGACGACGAGGATGGAAGCTGGGTTCCATGCAGGTGATGAACAGACCGCGGCG
 ATCATGAGGAGGCGGGGCGCACTTCATCAACGCTCTGCTGACCACCCCTGTGCTGCGCCCTCACGCTCCTC
 CATCTCTACTGGCAAGTACGTCCACAAACCACACCTTACACCAACATGAGAAGTGTCTCGCCCTCTGCGC
 AGGCACAGCAGAGAGCGCACCTTTGCCGTGTACTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG
 TATCTTAATGAATACACGGCTCTACGTGCCACCGGCTGGAAGGAGTGGGTGCGACTCTTAAAAACTCCCG
 CTTTATAACTACACGCTGTGTGCGAAGGGGTGAAAGAGAACGACGGCTCCGACTACTCCAAGGATTACCTCA
 CAGACCTCATCAACCAATGCAGCGTGAGCTTCTTCGCACTCCAAAGAAATGTACCCGACAGGGCCAGTCTCT
 ATGGTCATCAGCCATGCAGCGCCCCCAGGCGCTGAGGATTACGCCCCACAATATTACGGCTCTTCCCAAAAGC
 ATCTCAGCACATCAGCGGAGCTACAACCTACGCGCCCAACCCGGGACAAACACTGGATCATGCGCTACAGCGGGG
 CCATGAAGCCCATCCACATGTGAATTCACCAACATGCTCCAGCGGAGGCGCTTCGACAGCCCTCATGTCTGGTGAC
 GACCTCCATGGAAGCAATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACAGCTACATGATACACCGC
 CGACACGGTTACCAATTCGACGATTTGGCCTGGTGAAGGGAATCCATGGCATATGAGTTTATCAGAGG
 TCCCGTTCTACGTGAGGGGCCCCAAGCTGGAAGCCGCTGTCTGAATCCCCCATCGTCTCAACATGACCTG
 GCCCCACCATCTGAGCAATTGCGAGCCTGGACATACCTGCGGATATGGACGGGAATCCATCTCAAGCTG
 GGACACGGAGCGGCGGTGAATCGGTTCACTTGAAAAAGAAAGTGAAGGTCTGGCGGGAATCTCTTTGGTGG
 AGAGAGGCAAGTGCTACACAAGAGAGACAATGACAAGGTGGAGCCCGAGGAGGAATCTTTCGCCAAGTAC
 CAGCGTGTGAAGACCTGTGTGAGCGTGTGAGTACAGACGGCGCTGTGAGCAGCTGGGACAGAAGTGGCAGTG
 TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGAAGGGCCCATCGGGCTGGGCGGACGACAGGCC
 TCTCAACCTCTGCGCCAACTACTAGGGGAGGGCAGCGAGGCTGCACCTGTGACAGCGGGGACTACAAGCTC
 AGCCTGGGCGGAGCGCGGAAAAAATCTTCAAGAAAGAGTACAAGGCCCATGTGTCCGAGTCTGCTCATCCG
 CTCAGTGGCCATCGAGGTGGAGCGCAGGGGTGTACCACCTAGGCGTGGGTGATGCGCCGACGCCGAAACCTCA
 CCAAGCGGCATGGCCAGGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCATCGAGGCG
 TCTCCGACTCTCAGCGGCGCAAGTCCCTGAGGCTGGAAGACCAACAGCTGCACATCGACATGACAGCAAGTCCA
 GTGCAACAAATCAGCTACCAACCCGACCAAAAGGCGCTCAAGCAGAGGCTCCAGTGTGCATCTTTCAG
 GAAGGGCTGCAAGGAGAAGGACAGGTGTGGCTGTTGCGGGAGCGAGAGCGCAAGAAATCCCGACAGTGTG
 TCAAGCGCTGACAAACACGACCTGCGAGCATGCCAGGCTCAGCTGCTTCCAGCCCGACACACGACATGAG
 CAGACGCGCTTTCTGACGACTGGGCGCTTTCTGTGCTGCACACGCGCAACAATACACGCTACTGGTGAG
 GAGGACCATCAATGAGACTCACAATTTCTCTTCTGTAATTTGCACTGGCTTCTCAGAGTCTTTGATCTCA
 CACAGACCCCTACAGCTGATGAATGCGAGTGAACACCTGGACAGGAGTGTCTCAACAGCTACACGATACAG
 CTCATGGAGCTGAGGAGCTGCAAGGGTTTACAAGCAGTGAACCCCGGAGCTGAAACATGAGCTGGATGGAGG
 AAGCTATGAGCAATACAGGCACTTCAGCTCGAAAGTGGCCAGAAATGAAGAGACTTCTTCAACATCATCTGG
 GACAACCTGGGAAGGCTGGGAAGTTTAAAGTGAACATCGGTGCTACATCTTAGAAGACGACAGTCCA
 CTGCGAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACCTCTGTGATTTGGCCAGGAGGCTGACAAAGC
 AAGCAGCAGCTCTCAGTCAACATGACAGATTTCTGGAGGATACCCAGCAGGACGAGATACATTCAGGAAGTCC
 ATTTTGGCCCTGCTTTTGGTTTGGATTATACCTCACAGTGCACAAATGCAATTTTTCGATCAAAAGTCC
 ACCACTCAACCTCCCCAGAAGCTCAAAAGGAAACGGAGAGAGCGAGCGAGAGAGATTTCTTGGAAATTC
 TCCAGAGGGGAAAGTCAATTTGAAATTTTAAATCATAGGGGAAAGCAGCTCTGTGTTCTAAATCTCTTATTTCT
 TTTGTTTGTCAAAAGAGGAACATAAGAGCAGGACAGAGGCAACGCTGGAGAGGCTGAAACAGCTGACAGAGC
 TTTGCAATGAGTCAGTAGCAAAAGAGATGACATTTACCTAGCACTATAAACCTGGTTGCTCTGAAAGAA
 CTGCTCTCATGTATATATGTGACTATTTACATGTAATCAACATGGGAATCTTTAGGGGAGCACTATAAGAAAT
 CCAATTTTCAGAGGTGGTGTCTCAATAAACGCTCTGTGGCAGTGTAAAGAAAA

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MGFPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRNRIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFVTTMCCPSRSSILTKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPKHWMTRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGHYHIGQFGLVKGKSMPEYFDIRVPFVVRGNVEAGCLNPHIVLNLIDLAPTILDI
AGLDIPADM DGK SILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNKDVAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKGLKHCKGPMRLGGSRALS NLVPKY
YGGQSEACTDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHLKEHDEIETLQNKIKNLREVGRHLKKKRPEECDCHKISYHTQHKGRLKHRGSSL
HFFRKGLEQKIDKVLNREQRKHLKRLKLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLN
PFRACTSANNNTYWCMLRTINEKTHFLFCEFAFGLEYFLDNTDPYQLMNSVNTLGDRLVNLQ
HVQLMELRSCGKYQCNPRTRNMDLDGGSYEQYRQFQRKRWPEMKRPSKSLGOLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
 GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
 TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCCACC
 TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
 CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGGGGGCCACCTGGGAATCTTTCACC
 ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
 CCCCGCCACACCCTCACCACCTCCACCACCACCACCACCCACCACCACCATCCCCGCCA
 CGCTCGCTGAGGCTGCTGTGCGCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
 TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
 GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTAATATGGC
 AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGTTTGGGGAGTGGAGGCAAGG
 GTGCTCTTTCCGGGGTGGACAGCCCGTCTTGAGACAGTGACTCCAGTGAGCCCAGAAATG
 ACAAGCGTGCTTGCCAGAGCCAGCACACAAGTGATGTGAAGTGCCCGTCTTGACCTCCTC
 ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCTGAGAATGTCTTTT
 GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTTCATCGTGCCTTAGTCCAAGAAAAT
 AAAAAACCACTAAGAAGCTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRAPWPFER
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

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GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
CTACTGGGCTGATTGGGGCCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGGAASTGAGTGTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGTTGAGACTGGCGGCTTTTCACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCATCTGCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATTCTCGGCTGG
AGATCTACACGGAAGACAGCATTCATTTCATGTGCCCACTGGCAGCGGAGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCACTGCCACACTGTCACTGGGGCAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGAGCAGCAGCTACAGCAGTCAAGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCAAGCTGGACCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
ATGGCTGCACCCCTCTGCACTGCAGTTGCTGAGGAAGTGAAGAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCCTGAGGGACCTGACTTCCCTTGC
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA
GGAGCTATTTTCTGCACAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
ACAGTGTGAGCTCCAGGACCCAGAATAAAGCCAATGATTACTGTTTACCTGGAAAAAAA
AAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCavgSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRrvHPALDTYIKERKLCAYPRLEIYQEDQIHfMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSaatLSPGAS
SRGWDDGDTRSEHSYSESgASGSSFEELDLEGEgPLGESRLDPGTEPLGTTKWLWEPTapeK
GKE

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CCCGGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTCA**ATG**ACCCCTGCGCCCTCACTCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCTTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCCTCTGGTTATAGAACTTGCCCAAAGAGCAGGTGATTCAGGCTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCACTTGCCCTAT
GGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACATACTCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCCTCTGGTAG
GGATGGCCATGTGTCGACGCCCTCTGGGCTCATTGGGTACCACTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAAGAGCTCAAGGAAGAGAAACCAAGAGCAAAAAGAAAT**A**
ATAAATAATAAAATTTTAAAAAACTTAAAAAAAAGAAAAA

MTLRPSLLPLHLLLLLLLLSAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAPAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

CCCGGAACGTGTTCTCTGGCTGCCGACCCGAACAGCCTGTCTCGTCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCTCACTCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCTTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGTGCTTTTGGAGA
CACGCTTACATACATACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTTCTTCTACTTGGCCTATGG
AAAACGGGGATTTCACCACATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCTGGGCTCATTGGGTATCACCTATACAGAAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAAGAGCAAAAAGAAATAATA
AATAATAAATTTAAAAAGCTTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAATAATAAATTTAAAAAACTTAAAA

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CTGCTGCATCCGGGTGTCTGGAGGCTGTGCCGCTTTTGGTTTCTTGCCATAAAATCGGGGAG
TGAGGCGGGCCGGCGCGGCGACACCGGGCTCCGGAACCACATGCACGACGGGGCTGGACTG
ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
TATCATAGATGCAGCTGTTATTATCCCACCATGAAAGATTTC AACCTCATACCATGCCT
GTGGTGTTATAGCAACCATAGCCTTCTTAATGATTAAATCGAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
CTAAGAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
TTTGAGGGGCTGTTTTAAGTTTGGCCGCATGAAGACTTATGGCAGTGAACACATCTGAT
TCCCCAGGCACACAAGCCCTGATGGGTTTGGTTGTTTTTACTGCTCACTCCCAACCTT
TTGTAATGCCATTTTCTAAACTATTTCTGAGTGAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCATCTGATTAACCT
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGTTATAAT
TGTA AAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
CTCTCTGTGTCAAATGTTAATGAAATATAAATTTTTAGTTTTTAAATATTCCGTGG
TCAAATTTCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTCTGTGAACATGTAAT
GTAATCGGCTTTTGGAGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
GGTCCAGCCACCAAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
CAAGGGGAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCACCACGTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGAGTGAGGCGGGCCGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

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FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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FIGURE 62

GGGAGGCTGTGNCCGTTTTTGTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGTTCCGGGAACCATTCACGACGGGGTGACTGACCTGAAAAAATGTTTG
GATTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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FIGURE 63

CGACGCCGGCGTGA**TAG**TGGCTTCGGCTGGTGTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC
TCTCGAAAGTTTACTTTGGGACTATTCTCTGGCAGCTCCCGGAATCCCTTTCTCCGAAGATGTC
AAACGGGCCCCAGCGCCCTGGTAACTGACAAGGAGGCCAGGAAGGTTCTCAAACAAGC
TTTTTTCAGCCAAACCAAGTGGCCGAGAAAGCTGGATGTGGTGGTAATTGGCACTGGCTTTGGGG
CGCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGTCTGGAAACAACAT
ACCAAGGCGAGGGGGCTGCTGTCACTCTTTGGAAGAATGGCTTGAATTGCACAGGAAT
CCATTACATTGGGCGTATGGAAGAGGGCAGCATTTGCCGCTTTTATCTTGGACCATCTAGT
AAGGGCAGCTGGACTGGGCTCCCCCTGCTCTCTCTTTTACATCATGGTACTGGAAGGGCCCC
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTCAGGGCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCTCATGCCATCTCTGTGAAATTCCTCCCATTTGCCCTGGTTACGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTGCAGCAGCTGGGGCCCTCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCA
CTTACGGTGTCAACCCCAACACAGTGCCTTTCCATGCACGCCCTGCTGGTCAACCATAC
ATGAAGAGGGCTTTTATCCCCGAGGGGGTTCCAGTGAATTTGCCCTTCCACCATGACCTGT
GATTACAGCGGGCTGGGGGCGCTGTCTCACAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAAGCCTGTGGTGTGCTGTAAGAAGGGGCATGAGCTGGTGAACATCTATTGC
CCCATGCTGGTGTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
CCGCTGCTGCCAGGTGTGAAGACGCAACTGGGGACGGTGGCGCCGGCTTAGGCGATGACCT
CTGTGTTTCATCTGCCCTGCGAGGCACCAAGGAAGACTGCATTCGCCCTCCACCACTACTAT
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGCTCCATGCCACCCAGGAAGA
GGCTGCGGAACACATCCCTCTTCTCTCTCGCTTTCCCATCAGCCAAAGATCCGACCTGGGG
AGGACCGATTCCAGGGCCGTCCACCATGATCATGCTCATACCCACTGCCCTACGAGTGGTTT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGCAGTGAATAGACCTTCAAAAACCTC
CTTTGTGAAGCGCTCTATGTACAGTGGTCTGAAAGTGTTCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTCACCACCAAGTCTTATCTGGCTGCTCCCCGAGGTGCC
TGCTACGGGGCTGACCATGACCTGGGGCGCTGCACCTTGTGTGATGGGCTCCTTGAAGGG
CCAGAGCCCTTCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTGTGGACTGGTCTG
GGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGCGCATCTGAAGCGGGAATGTACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAA**TAG**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGCAGGTATAAAGCACTCTAATTTGGTTCTGATGGCTGAAGAGAGGGCTAG
TTTAAATCACAATTCGAAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTTGATG
TCTCATGACGAGCGGGCTCTGCATCCCTCACCCTGCGCTCCTAACTCAGTGATCAAAGCGA
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGCTCAGCTCAACCTGGTGGGTTCACTTC
TGTCTGAGGCTTCTGCTCTCATTTCAATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAGGGGAGACTAATGAGGCTTAACCTCAAACACTGGGCGTGGTTTTGGTTGCCATTCCATA
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCACTGGCTCTTCAGGGGACAGGAAT
GCCGTGTGCTGGCCAGTGTGGTTCTGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTGAGTATCATATCAATTCATATGGAAGTCCCGGGTCTGTCTTCCCTTATCA
TCGGGGTGGCAGTGGTTCTCAATGTGCCAGCAGGGAAGTCACTGAGCTGAGCCTCAATCAAGC
CTTATCCACCAATACACAGGGAAGGGTGTGGGTGAAGGAGGGAAGTCAATCAAGGAAGGGA
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTTGCAGTTAATTAGCAGATGTGAGGG
TTAGACGGTAGGTGATCAAGCTCAAGTTTGGAAAAATGACTTCTCAGTTATGTCTTTT
GTATCAGACATACGAAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAATTTATTG
ATTCCATTGCTTTAAAAA

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FIGURE 65

GCAGCGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTTGGCACCGGCCCGGAGAGGAGGGATGCGGGTCCGATAGGGCTGACGCTGCTGCTGTG
 TGGGTGCTGCTGAGCTTGGCCTCGGCGTCCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAAGAGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG
 AGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGAAAACAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCTTTTCTTTTCTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC
 TCTTGGCTTTCTGTATGCCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGAT
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTGTGGTTTATAGCGCCACAACTTTT
 TCAGCTTTCATGATCCAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACTTCCTTCAA
 ATCTTGTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA
 ATTTTTCTTTAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTTAAATTTTCTCTGAGTTGGAATTGTCAGAATCATTTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT
 GTGCAAGATGACTCCAGAGAGCTCTACTTTCTGTTTTTACTTTTCATGATTGGCTGTCTTC
 CCATTTATTCTGGTCAATTTATTGCTAGTGACACTGTGCCTGCTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTTACTTTTCTTTGCTAATTTGGAAGATTAACTCATTTTTTAATAAA
 ATTATGTCTAAGATTAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEFPKKVRKPALTAIEGTAHG
EPCHFPPFLFDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAKRRQMQAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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CTTCCAGCCCTGTGCCCCAAGCACCTGGAGCATATAGCCTTGCAAACTTCTACTTGCCT
GCCTCCCTGCCTTGGCCATGGCCTGCCGGTGCCTCAGCTTCTCTGATGGGGACCTTCC
GTCAGTTTCCAGACAGTCTGGCCCCAGCTGGATGCACTGCTGGTCTTCCAGGCCAAGTGG
CTCAACTCTCTGACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGCTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCTGTGACATCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGTGTGAGATGGGTGCCCTCCCCTCTGCCTCCATTCT
GCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 68

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQVQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSF

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FIGURE 69

GCGGCCCGCCCCGAGACCGGGCCCGGGGGCGCGGGGCGCGGGATGCGGCGCCCCGGGGCGG
 CGATGACCGCGGAGCGCAGCGCGGGCCCGGCCCTGACCCCGCGCCCGCCCGCTGAGAGCCC
 CCGCGCGAGGTCGCGACAGGCCGAGATGACAGCGCGAGCCCTGTTGCTGCTGCTGCGCGC
 CGCTGCTGCTGGGGGCCCTTCCACCGCGCGCGCGCGCCGAGGCCCGCCCAAGATGCGCGAC
 AAGGTGGTCCACCGGAGGTGGCCCGGTGGGCGCACTGTGGGCTGCAGTGGCCAGTGGG
 GGGGCGACCCCGCGCGCTGACCATGTGGACAAAGGATGGCGCGACCATCCACAGCGGCTGGG
 GCGGCTTCCGCGTGTGCCGAGGGGCTGAAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCGTGAAGCTCAACTACACCCCTCGTGT
 GCTGGATGACATTAGCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCTCTGGGGGTCAAG
 AGGACCCCGCCAGCCAGCAGTGGGCAAGCCGCTTCACACAGCCCTCCAAGATGAGGCGC
 CGGGTGTATCGCAGCGGCCGTGGGTAGCTCCGTGCGGCTCAAGTGCCTGGCCAGCGGGACCC
 TCGGCGCGACATCACGTGGATGAAGGACGACAGGCCCTTGACGCGCCAGAGGCGGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGCCCTGAAGAACCCTGCGGCGGGAGACAGCGGCAAAATAC
 ACCTGCCGCGTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAAGTGGATGTGATCCA
 GCGGACCGGTTCCAAGCCGTGCTCACAGGCGACGCCCTGAACACGACCGTGGACTTCG
 GGGGAGCCACGTCCTTCCAGTGCAGGTGGCGAGCGACGTGAAGCCGCTGATCCAGTGGCTCG
 AAGCCGCTGGAGTACGGCGCGAGGGCCGCGCAACTCCACCATCGATGTGGGCGCGAGAA
 GTTTGTGGTGTGCTCCACGGGTGACGTGTGGTGGCGGCGCGAGCGCTCTCACTCAATAAGC
 TGCTCATCACCGGTGCGCGCGAGGACGATGGCGGCTGTACATCTGCTTGGCGCCAACACC
 ATGGGCTACAGCTTCCGCGAGCGCTTCCTCACCGTGTGTCGACGCCAAACCCGCGAGGCGC
 CCGCTGGGCTCTGCTGCTTCCGCGCACTAGCCTGGCGGCGGCTGGTCTCGGCTCCGATCCGAG
 CGGCGGCTGTCTTCATCTTGGGCAACCTGCTCTGTGGCTTTGCCAGGCGCCAGAAGAAGCG
 TGCACCCCGCGGCTGCTCCCTCCCTGCTGGGACCGCGCGGGGACCGCGCGGCGGACCG
 CAGCGGAGACAGGACCTTCTCTGTTGGCGGCTTCAGCGCTGGCCCTGTGTGGGGCTGT
 GTGAGGAGCATGGTCTTCGCGAGCCCCCAGCACTTACTGGGCGCGGCGGCGGCTGTCTGGC
 CCTAAGTTGATCCCCAACTCTACACAGACATCCACACACACACACACACTCTCACAC
 ACCTACACAGCTGGAGGGCAAGGTCCACAGCACATCCACTCATAGTGTAGAGCGGACCGGT
 ATCTGCAGTGGGCGAGGGGGGGCGGCGCAGACAGGCGAGCTGGGAGGATGGAGGAGGAGCT
 GCAGCGAAGGCGAGGGGACCATGGCGAGGAGGAATGGCCAGCAGCCCGAGCGAGTCTGTGTG
 TGAGGCATAGCCCTGGACACACACACACAGACACACACTACTGATGCATGTATGCAC
 ACATGCGCGCGACAGCTGCTCCCTGAAGGCACACGTACGCACACGACATGCACAGATATG
 CCGCTGGGCGACACAGATAAGCTGCCAAATGCACGCACACGCGACAGAGATGCCAGAAACA
 TACAAGGACATGCTGCTGAACATACACACGCAACCCATGCGCAGATGTGCTGGGATACGACA
 CACACACACACACGGATATGCTGTCTGGACGACACACAGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCTGGACACAGATAATGCTGCGCTTGACACACACATGCACGG
 ATATTGCTGGACACACACACACACACGCGTGCACAGATATGCTGTGCGACACGCGACAC
 ACATGCAGATATGCTGCTGGACACACACTTCCAGACACAGTGCACAGGCGAGATATGCT
 GCCTGGACACACGAGATATGCTGTCTAGTACACACACACGCGAGCATGCTGTCCGGACAC
 ACACACGATGCACAGATATGCTGTCCGGACACACACACGACCGACAGATATGCTGCTGGAC
 ACACACAGATATGCTGCTTCAACACTCACACACAGTGCAGATATGCTGCTGGACACACACA
 TGTGACAGATATGCTGTGGACATGCACACACAGTGCAGATATGCTGCTGGGATACACAGC
 CAGCGACACATGCAGATATGCTGCTGGGACACACTTCCGGACACACATGCACACAGGT
 GCAGATATGCTGCTGGACACACACAGATATGCTGCTTCAACACTCACACAGTGCAGATATG
 TATTGCTGGACACACACATGTGCACAGATATGCTGTGAGACATGCACACAGCTGCAGATA
 TGTGCTGCGGATACACACGCGACACATGCAGATATGCTGCTGGGACACACTTCCGGA
 CACACATGCACACAGGTGCAGATATGCTGCTGGACACACGAGATGACGTGCTTGTGG
 GAGGTGTGCGGTGAAGCCTGCAGTACGTGTGCGGTGAGGCTCATAGTTGATGAGGAGCTTT
 CCGTGTCTCCAGCTGACTCCCCAACTCTGCGCGGCTCTGTCCCGGCTCAGTCCCCGGCTC
 CATCCCCGCTGTCTCCCCCTGGCGGCTATTTTGGCCACTGCTTGGGTGGCGGAGG
 AGTCCCGCTACTGCTGTGGGCTGGGGTTGGGGGCGACAGGCCCAAGCCTGAGAGGCTGGAG
 CCGATGCTAGTGGCTCATCCCCAGTGCAATTTCCCGCTGACACAGAGAAGGGGCTGGATA
 TTTATATTTAAGAAATGAAGATAATATTAATATGATGAAGGAAGACTGGGTGTCCAGGGAC
 TGTGCTCTCTGCTGGGCGCGGGACCGCGCTGCTTTCAGCATGCTGATGACACACCCCG
 GTCCAGGCGACACACACCCCGGCGGCGGCTGCTGCTGGTGGCGGCGAGATCTCTGTAATTTTA
 TGTAGAGTTTGAGCTGAAGCCCGGTATATTTAATTTATTTTGTAAACACAAAA

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MTFSPLLLLLLPLLLLGAFPPAAAARGPPKMDKVVPRQVARLGRTVRLQCPEVGDPPLTMT
WTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFSGLSVNYTLVLLDDISPGK
ESLGPDDSSSGQEDPASQQWARPRFTQPSKMRVRVIARVPGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPVLT
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGHRNSTIDVGGQKFFVLLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLTLLWLCLQAQKKPCTPAPAPPLPGHRPPGTARDRS GDKDLPS
LAALSAGPGVGLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHIHYOC

[illegible]

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESFGEWTTWFNI
 DYPGGKGDYERLDAIRFYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSFREGFWCLNREQ
 RPGQNCSTNYTVRFLCPEPGLRRDTERIWSPPSPWSKCSAACGQTGVQTRTRICLAEVSVLCS
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMQDFMLHGAVSLPGGAPASGAIIYLLTK
 TPKLLTQTDS DGRFRIPGLCPDGKSILKITKVKFAPIVLTMPTKSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNFVPESYLIRLPHDCFQATNSFYVDVGRCPV
 KTCAGQQDNGIRCRDAVQNCGISKTEEREIQCSGYTLPTKVAKECSCQRCETETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
 KKGSVAFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPNISTATAAQDTLNFINDGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSEERFLPSEIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGNGA
 CVPAFCDQSPDAYSAIVLASLAGEELQAVESSPKFNPNAIGVFPQPYLNKLNRYRRTDHEDPR
 VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDNTVPFN
 EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVI PQGSCRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQS PAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPVRA
 QQPLIN

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CTCGAAGTTGTTAAACGCCAACACACAAGTAGTGTAGGCTTCCACCAAAGCTCCTCAATATACCTGAATACGCAC
AATACTTCAACTCTTCATATTTGGTTTGGGATCTGCTTGAGGTCCCATCTTCATTAAAAAAAATAACAGAG
ACCTACTACCCCGTACAGCTATACATATCATATGTGTATATATGTATGAAATGACAGAAAGTCAGGATCAATAAGG
AAGCTCTGCTTTAGTGTCTCAAGAGAGATTAACAAGAAATTTAGACATGATTTTGTCAAGATCCCTGTGCATTCATG
CCCTTTGGGTTCAGGTGTCTCAGTAGTGACGACCTACCTTTGGTTGGGGACATATGATTTGTGTGTAGACT
CAGATTTACACGGGAAGAGGGAAGTTTGGGATTCATGGTCCGACCGGAGATCCACGGCAATGACAAAATA
TCTGAAAGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCTCTCGAGAGCTCTGTGCAATGGGCAAT
CTCTACATGTGCAATATGAGTGTGATGGAGTACCCCTGAGCTGGCACAACCCCTGAGCTGATGTTGATTTT
TCAAGGAAGACATCCCTCCATATTTGGCACTCTGCCACTTGGAAAGGATATCCAAGCTCTCCAGGTTAAACAT
CACTCTGTCTTGAGGACAAAACATTTGAGCTACACGACACAACTAGTTATTACCTTTGAACTTGGAGCTGGGCGTCAGAC
AATATGATCTGGGAGAGTCTCTCGATTGAGCAGACATGGGACGATTCAGTATTTATGCCACAGACTGCTTAA
GAGTGTCTCAACGTGATCTCAATCCGTGAAGGATTTACAGCATACGGTCTTAGAATATTTTGATTTTGACAGACA
AGAGTTTCAACAGGTTATACACCAATAGCAAAATACTCCATTTGAAATCAAAGCAGGTTTCGGCTTTTGTG
CTGGACCTCGCCTACGCAATATGGTCTCCCTCTACGGACAGCTGGTATACCAACGAAGAACTCAGAGATTTTGT
ACAGTACAGACATCTGAGGATAGGCTGTGAAGACCGCGTTGGGAAATATTTGTAGTAGCTACACTTTGGC
AGCTACTTTTACGGCATCTCAGACATAAAGGTGGCAGGAAGGTGCAAGTGTAACTCCATGCCACTGTATGTGTG
TGATGACACAGCAAAATGACATCGAATGTGAGCACACACTACAGGTCAGAGCTGTGGGAATGCAAGAAG
AATTTATCAGGGCGCACTCTGGAGTCAGGCTCCTTATCTCCCATCCCAAGGCACTGCAAAATACGTGTATCCC
CAGATTTTCCAGTATTTGGTAGCAATGTCTGGCAGAACAGGCTCTGTGCACTGCCAGAACGGGAGGACGTGCCACA
CAAGCTGGCGTCCCTGTGGCGGGCCGATACACGGGATCTCTCTGCGAGAGAGCTCGGCTGGAGGAGGCTGGC
AGCTCGGCTCCGACTCTGGCAGGGGGCGCCCGGACCGGCCACAGGCTGCTGTGTGTCGACAGCTGCTGT
GGGAACCGCGACGCCCTTGTTGTTCTAGAGTGTACCTCAGCCACACCGGACGGGCTGTGCGTGGGGAAGCA
GACACAAACCCAAACTTTGTACTATACATAGGAACACACATACAGACACCCCACTGACAGTGTACAAAT
CTAAGAAAGGCTTAAGTGAATAGCCATATTATCACCGTGGACAGACACATCCGAGTCAGACTGTAAATTTG
TGACTGAGGAGGATTTGGCAGTGTGTATATTACTGCAAAATCAATTCGCACTCGAGAGCTTTGTTGGT
TTGGAAAGGCTGCGACGCCCCCCAGGAAGACAGAAAACAAACAAATCAACCGCACTAAAAACATTTGGC
TACTCTAGCTGGTGGTGACCTAGTACGACTCCGCCAGTGTGGACACACAAATAGCAATCTTTGCTGTGAC
GTGCTTTGTGGGATATAGGAATACTGTGTAACAGTCCGATTTGGCCTGCTTCGCTCGCTGATCCCTTCCAC
TGTGCTTTTGTGAAGCTTGCTCTGTAACCTCTGTGTTTGAAGAGTTCTTTGTGCTGATGTAGTGTGACACA
CTGTGTAAACGGCCCCCTTAAGAGCGCAAGGCTCATACCCCTGTATCTTTAGCAGACTGAGTCAGTCCGTCGA
GCACACACCCCTATACAGAGGTGCTCTATAGAAAATAAGAGTGTATCTATCTTTGTATCTAAATGAAGTT
ATTTTCTGTGAATCTGATATATGTAGATTTTGTATATTTGCCAATTTGGTTTACGACACATCTGTTAAT
GTATCTAATTGGAATCAGCAAGAGCTGACATTTATTTGTGCTCTTCTGCTGTGTTTGTGTTTCACTGTGACA
GATTTCTCTGTAAAGGCGACAGCAAGCTGCTGGCATCAAAGATATCATGTTTACATATATACAGAGTGAATAGCA
TTCCACCAAAGGCAATCTTAATGTTTCTTTGTGCTTTAACTGGAAGATTTAAAGAAATAAAACTCTGCA
TAAACGATTTTCAGGAATTTGTATGCAATTTCTTAAGATGAAGAGACAGCCACCAAGCATTTTACACTCT
TTACTGATTTCTGTGTGGACTGATGACTTCTCAGCTACGAAATTTAGTTCGGAGAAATGATGATGTGTTCACT
AGCTTGGACACTCTTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACACAGCAAAAAAATAAATAA
AAAAAATA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFFTVTDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDGCKCKKNYQGRPWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLTGAS
PLVF

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CCACGCGCTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGGCCG
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCGCGGCAGAGTGTCTCATGACTT
CTCTTGTGGACC**ATG**TCCGTGATCTTTTTTGCCTGCGTGGTACGGTAAGGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTGAGAGTTCTGCAGAAGTTGTGACTTT
AGTATACATTTTTCTTCTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTC
AGCAGCCATGGCCTTCTGCTTCTCGGAGACCTGTGGTGGGAATTCACAGCTTCTATGACA
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATATTAG
AAAGTGAAGTGGCATTTTAATATGTAAGTTCCTCTCAGATGGAGTGACGCTTGGAAAAAT
TCAGGAGGAGCTCAAGTTCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
ATGGGGTGATGAATGGTCACACCCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
CCAGTGACAGCCCTGGGTATCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
CATTCTGAGGAGTTACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGTTCTGCTGGT
TGGACCAAACTCT**GTA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGAGCCTGTGGA
AAAGGCATGTGCAAGTAAATCTGGGAATGGCTGGATTGGAACATCTGCCATGTGTATTG
ATGGCAGAGCTGTTGCCACAAAGCGCCTTTTATTAGGGTAAAAATTAACAAATCCATTCTAT
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTACATTTATATGATTCTGGGGTT
GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTTGATCCCCCAGGATTCTATTTGT
TTAATGGGCTTTTCTACTAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTC
TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAAACTCAGTAGTACAACC
TAAACTTGATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
AAGTGGCTTCGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAAA
AAAAG

FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF
SSFGDVACMAICSCQCPAAMAFCFLET LWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAGAAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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CTCAGCGCGCTTCCCTGATAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA
CCCCGACCTTAAAGAGCTGGGGAGCAAAAGGGAGGACAGAGCCCTTTAAACACGAGGCGGGTGTTG
CTCGCCCTTTAAAGGCGGGGCGTCGGACGACTGTATCTGAGCCCCAGACTGCCCCAGTT
TCTGTTCGCAAGGCTCGCAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGGCGCGGCTT
CTCTCCCGCTCGTCTCTCCCGGGCCAGAGCCGCTCGGCTTCAGTATGCTGAGCAGAGTA
TGGAAGACCTTGACTACGAAGTGCTATCGGTCGCAGAACAGTATTCCACGAGAGGATCCGC
GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCTCTGCCACATCTTCTCTGA
CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGCTGGATGATGAAGATGCCACCGTCAACAGA
TGGCGTGCAGCTGTGCACCTTTACCTTGGCAATTGCCCTGGGTGCTGCTGCTCTGCC
TTCTCTCATCATCAGCAATGAGTGTCTGCTCTCTCCCTGCCCTCGGAACACTACATCCAGTGGCT
CAAGGCTCCCTCATCTCATGGCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTGA
TCTTCTCATGCCCTTGCATATTTCTTCACTGAGTCTGAGGCGTTTGTGCTGCTCCAGAAG
GGTGTCTGGGCGGGGTCTATGAGACAGTGGTGATGTTGAGTCCCTCACTCTGCTGGTGC
AGGATGGTGTGGGTGCATCAGCAATTGTGGACAACGAAGGCCAACAGAGATCACTCT
ATGACTTTTGGGAGTACTACTTCCCTACCTCTACTCATGCATCTCCTTCTCTGGGGTTCTG
CTGCTCTCTGGTGTGTAATCCACTGGGTCTCGCCGCGACTGTCTCCGTCAGCTGGGAAGCTGCT
AGTCAAGCCCGGCTGCTGGAAGACTCGGAGGACAGCTGTACTGCTCAGCCCTTTGAGGAG
CAGCCCTGACCCGAGGATCTGTAATCTTACTTCTGCTGGCTGCCTTTAGACATGGAGTCT
CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGCTCTGCTGGAGAAGGCGGAAGGC
TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTCTTGTGGTGTGCTACGG
CGCTGTCTGTGCTCATTTGTGCCATCCACATCTCGGAGCTGTCTATCATGAGGCTGCCATG
CCCCAGGACTCGAGGTTACTCTTATGGCCAGTCTCTCTTCTCAAGCTGGGCTCCTTTGG
TGCGTCTATTGAGTTGTACTCATCTTTTACCTAATGGTGTCTCTCAGTTGTGGGCTTCTATA
GCTCTCCACTCTTCCGAGGACTCGGGCCAGATGGCAGCAGACTGCCATGACGCAGATAATT
GGAACTGTGTCTGTCTCTGGTCTTAAGCTCAGCACTTCTGTCTCTCTCGAACCTCTGGG
GCTCACTCGCTTTGACCTGCTGGGTGACTGTTTGAACGCTTCAACTGGTGTGGGCAATTTCTAC
TTGTGTCTCTCTACACGCGCCTTTGACGGCTTCACCACACTGTCTGGTGAAGACCTTC
ACTGCAAGCTGTGGCGGCGAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCGCTGCCGT
CTCGGTTTCCCCAGGCATCTAGGAAGAACCCAGCAGCAG**GAC**CTCCAGTGGGGGTGGGA
AGGAAAAAAGTGCACATGCCATCTGTCTGCTTAGGCCTGGAGGAGGCCAAGGCTACTTTGG
ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGCCATCTGCACATT
GCATAATCTGAGGACAGAGTTTGGGACAGGACCTCTCTCTTTCCATACTTAAGTGTGGCC
CAGCATGGGTTAGGGCTGGGTGACTGGGTCTAGCCCTGATGCCAAATCTGTTTACATATCA
ATCTGCCCTGACTGCTGTTCTGGGCGACTCCCATAGCCATGTTTACATGATTGTATGTCAT
AGGTTGGGTTAGGGCAGGGAAGGACTGGGCGAGGCGAGGCTCGGGAGGATAGATTGTCTCC
TGTGGCTCTGGCCACAGAGCGCTAAGCACTGTGCTATCTCGAGGGGCTTTGGACCACTG
AAGAACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAGTTGATCCAGGGA
AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLVLGMOVVVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRLLDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLSFGAVIQVVLIFYLMVSSVVGIFY
SSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY
IVFLYNAAFAGLTTICLVKTFTA AVRAELIRAFGLDRPLPVS GFPPQASRKTQHQ

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAAACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGCCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

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GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGTGCTGT
GGGTGATATTACTGGTCTGGCTCTGTCTAGTGGACAGTTTGCAAGGACACCCAGGCCATT
ATTTTCTCCAGCTCCATGGACCACAGTCTTCCAAGGAGAGAGTACCCCTCACTTGCAA
GGGATTTGCTTCTACTCACCACAGAAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTTCAGAGATGGGATTTCC
TCATGCTGCCAGGCTAATGTTGAACTCTGGGCTCAAGTGATCTGCTCACCTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCTGCAAGCTCCACTTTCTGTGTTGAAGGAGAC
TGTGTGGTTCTGAGGTGCCGGGCAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGTAAATGTCTTGGCATTCTTAATAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGGFPHAAQANVELLGSSDLLT

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FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCTCACAGGCGCGGTGGGCTGGCGAGCCGACGCGGCGGAGGAGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGACTTGA
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAGGCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGAACCTGATGATCCACAAGCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGTTCTGTGAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACCTTGAAGAAGTATATGCAGGAAATTTTGTGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCCGCAAGAGAT
 GCGGACCAACCGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGAGCCTGG
 AGATTTACGGTCCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACGAGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACCTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTGACTTTGTTTAAATAAGTGAATAAGCGATATTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTGTTTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTCATTGCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT
 TTCAAGAAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTAGCAATTTATTCAAATGCCAAGTGGAGAAGTCTGTTTTTAAATACATTTTGTGTT
 TTATTTT

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKIALQLHPDRNPDDFQ
AQEFQDLGAAYEVLSDSEKRKQYDTYGEGLKDGHQSSHGDI FSHFFGDFGMFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRCQEMRTTQLGPGRFQ
MTQEVVCECPNVKLVNEERTLEVEIEPGVRDGMIEYPFIGEPEHVDGEPGLRFRIKVVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCGTGTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG
CCTATAGGAACTAGCCCTGCAGNTTTATCCCGACCGGAACCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTTAAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

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FIGURE 87

GGCACGAGGCGGCGGGCAGTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT
CTCTGCAGGTGTCTGGAGGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCA
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGCATGG
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGACAGCC
TTGGTGCTGGTTTGACAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
TAAGCCCATTTGTGGACCTCATTTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
TGGACGATGTCTGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTGAAGATTTGTACACTCTGAC
AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
GCGACATCATTGTGGTGCCAAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
TACCCTCCGTTGGACCCCAAACCTCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCAG
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTTAGTGCCT
ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTACAGCTGTGTGTGCATAG
TAAAGCAGGAGATCCCGTCAGTTTATGCCTCTTTTGCAAGTTGCAAACTGTGGCTGGTGAGT
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
CTGGTGGACTGTGAGCTTTATTTAGCTCACCTAGTGTGTTTCAAGAAAATTGAGCCACCGTCT
AAGAAATCAAGAGGTTTACATTAAAAATTAGAATTTCTGGCCCTCTCTCGATCGGTGAGAATG
TGTGGCAATTTCTGATCTGCATTTTCAAGAGGACAATCAATTGAACTAAGTAGGGGTTTCT
TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGTTTGGGTTTGAAGCTGAGGAACT
ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
GATAGTAAATTTATACCTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCC
 CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATGGTTAGAAAGAACATTGAGAT
 TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGTATTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTGTTCAG
 GGGCTTCTTCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
 AGTGAATTTGAAGACTCATTTAAATATTTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCTGTTTCTTTTCTTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTTAAACCAAGGAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MSISLTDTKQKIGMGLTGFVGFLLFFGMILFFDKALLAIGNVLVAGLAFVIGLERTFRFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFLLFRGFFPVVVGFIARRVPVLGSLNLNPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTCCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAATTGTTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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FIGURE 92

GGACAGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCCTTCTGAGTCTTGGATCTTTCTTCTCTGAAATCTTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGACCTCGCGGGACTGC
 TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
 ATCAACACCATTACAGTCTTCACTCTCTCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATTCTCACGGACCCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGCTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTTGCAGACCTCCGGGACTACCCCGAGAAGTATTTTTCTCT
 GATTCAGTGTAGGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTTCAGAAA
 TAATGAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGTCTGGCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCAGAG
 GACGCCCATGGTGCCCCCGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCCTCGC
 TGGTGCTCTACCCCTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTCATCTCTGCTCTTCTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
 GACTCAGGAGGTGTACCATCCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGATGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCCTGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGTGAGTGTGAACCTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGACCGAAGGGGACAGTTCCCTTTTCATCCTTTGTGTGTGAGTTTTCTGT
 AACCTTGGTTGCCAGAGATAAAGTGAAGTGTCTTAGGTGAGATGACTAAATATGCCTC
 CAAGAAAAAAAATTAAGTGTCTTTCTGGGTCAAAAAAAAAA

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FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVNLGKK
YHADLYVRRIPLEDDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRRMIGVTEIDKGSAYGNSDS
KQKLND

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CTGAGGCGCGGTTAGC**ATG**AGAGGGGAGAGTACGTCGGCGGTTGCTCTCGGGCTTTTGTGCTCG
GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAA
GTAAAGGTGAAGCCAAGAACAGCATTACTGATCCCAAATGGATGATGTTGAAGTTGTTTA
TACAATTGACATTAGAAATATATTTCCATGCTATCAGCTTTTTAGCTTTTATAAATCTTCAG
GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAAATGTGGTAGG
TGGTACAAAATTCGTCGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACA
AAACTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACACCAAGTATAA
TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCCTGAACAACTGGGTTATAAAAC
TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
TTTTTGAAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
CAAGAGGAATTAAGAGATATATGCAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
AGTAAGGATGTAAACAGATATTAACACGAGAATTGAGAAAAGGAGGACGAGGCACAGATT
CAGCAAGAGAGAAGAACATCCAAAAGACCTCAGGAGAACATTTTTCTTTGTCCAGGCATTA
CGGACCTTTTTTCCAATTTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
TGTTTTCTAAAGTAGCTGTAACACAAACCACCTCTCGATGTAGTAGACAATCTGACCTTAA
TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT
AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
CAAACGATCTAAAGCAAATCTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
TTTT**TGA**TCCTTTTAACCTTACAGGAGATTTTTTTATTGCGTGATGGGTAAAGCCAAACAT
TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTTTTTACTATGTTCAC
CTGTTTGCAGTAATACAGATAACTCTTAGTGCATTTACTTTCACAAAGTACTTTTTCAAAC
ATCAGATGCTTTTATTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCT
TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
TCCAGCAGCTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
TGGGCAACGATATTGAGACCATTGCTATTAATAAAAAATAAATGGAAAAGCAAGAATAGCCTTAT
TTTCCAAATATGGAAGAGAAATTTATATGAAATTTATCTGAGTCAATTAAATTTCTCCTTAAG
TGATACTTTTTTAGAAGTACATTAATGGCTAGGTTGCCAGATAAAATGTGGATATCATGCA
ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLEVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHREHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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FIGURE 96

GGCACAGCGCGCGGGCGAGAGTCAAGCCGAGCCAGTCCAGCCGGACGAGCGGACACGCGCAGGGCGACG
 CCAAGCAGCGCGCAGCGAAGCGCCCGCCGCGCCACACCTCTCGGCTCCCGCGGGCGCTGCCACCTTCCCT
 CCTTCCCGCGCTCCCGCCTCGCGGGCAGTCAAGTTCGCGGGTTCGCTGCCCGCGAAGCCCGAGGTCAACCA
 GCGCGCGCTCTGCTTCCCTGGGCGCGCGCGCTCCACGCGCTCCTTCTCCCTGGCCGGCGCTGGCACC
 GGGGACCGTTCGCTGACGGGAGGCGCAGCTCTACTTTTCGCGCGCGCTCTCCTCCGCTCTCGCCTTCTCCAC
 CACTCCCACTCTCTCCCTCCAGCTCCACTCGCTAGTCCCGACTCCGCGACGCTCGGCGCGCTGGCGGTAG
 CGCGCTTCCCTCCGCTCCAAAGTGGGAACGCTCCGCGCGCGCGCACATGGCACGGTTCGGCTTCC
 CGCGCTTCTCTCACCTTGGCAGTCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAGTTGCTCGG
 AACTGCGAGCTCTTACGTCTCAAAGGCTTCAAGAAGACGATGCCCGCTCCACGAGATCAACGGTGTATCAT
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGAATCATTTGCAAGCTGTCTTTGCTTACGTTACAAGAAAGTTTG
 ATGAATTTCTCAAAGAACTACTTGAAGATGAGAGAAATCCCTGAATGATATGTTTGAAGACATATGGCCAT
 TTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAAGAAATGCTAAATGACTTCTGGGCTCGCCTCTGGAGCGGATGTTCCGCGCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTGCTTTTGAGCAGCCGCTACTTTCGCTCAAGGCTTACGCGTTGCGGG
 AGATGCTGTGAGCAAGGTCTCGGTGTTAAACCCACAGCCCGAGTGTACCATGCCCTGTTGAAGATGATCTACT
 GCTCCCATGCGCGGGTCTCGTGACTGTGAAGCCATGTTACAACACTGCTCAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATTAATCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTATTTATGAACATCGAGG
 ATAATAGTGTTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCGCAAGCCCTCCAGCTGGACGAAT
 TCTCGTTCCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCAACACAGC
 AGCTGGCACTAGTTTGACCGGCTGTTACTGATGTCAAGGAGAACTGAACAGGCGAAGAAATCTGTGCTCT
 CCCTTCCGAGCAACGTTTGCACAGATGAGAGGATGGCTGAGGAAACGGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACTGTTTGCAGTGACAGGAAATGGATTAGCCAACAGGGCAACACCCAGAGGTCCA
 GGTTGACACCGCAACACGACATACTGATCCTTCGTAACATCATGGCTCTTCGAGTGATGACCAAGAGATGA
 AGAATGCATACAATGGGAACGACGTGGACTCTTTGATATCAGTGATGAAAGTAGTGGAGAGGAAGTGGAAAT
 GGCTGTGATATCAGCACTGCCCTTCAGAGTTTGACTACAAATGCCACTGACCATGCTGGGAAGAGTGGCAATGA
 GAAAGCCGACAGTGTGGTGTCCGCTCTGGGGCAGCGCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGG
 TTTATGCAGAGAGAGTGGAGATTAATTTCTCAAACCTGAGAAAAAGTTCATCAAAAAGTTAAAGGCACCACTG
 ATCACTTTTCTACCACTCTGACTTTGCTTTTAAATGAATGGACAACAAATGTACAGTTTACTATGTGGC
 CACTGGTTTGAAGAAGTCTGACTTTGTTTTCTCATTACGTTTGGGAGAAAAAGGACGTGCTGATTGAGTTGGT
 TCTCTCTCCCGCAACCATGTTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA
 TTTTATCACTCTAATTTGTTGTATGTTTTTTTCTCATTTCGTTTGTGGTTTATTTTCCAACTGTGAICT
 CGCCTTGTCTTACAGCAACACGAGGTCCCTCTTGGCAGTAACATGTAGTATTTCTGAAATTTAAATA
 GCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

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MARFGLPALCTLAVLSAALLAAELKSKSCSEVRRLVYVSKGFNKNDAPLHEINGDHLKICFQ
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLVQMNSLFLKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFLVNSQYHFTDEY
LECVSKYTEQLKFPFGDVPRKLKLQVTRAFFAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGFPNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGCGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTVKEKLQAKKFFVSSLSLNVNCNDEMMAAGNEDDCWNGKGKSRYL
AVTNGLANQCNPNFEVQDVTSPKDFILRLQIMALRMTSKMAYNGNDVDVDFISDESSE
GSGSGCEYQCPSEFDYNATHDAGKSANEKADSAGVRGQAQAYLLTVFCILFLVMOREWR

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAGTCTTAATCTCTTCCCTCCTCTGTTGC
TGCCACTAATGCTGATGCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAATGTGAGTGCAA
AGATTGTTTCTCTGAGAGCCCCGAGAAGAAAATTATGACAGTGTCTGGGCTGCCAAGAAGC
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAAAAGACACCAAAGGCACCCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCCACTGTACCCACC
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTGTGCTCT
TCTAGTGCTCTTCTCTCTCGTAGCTCTTAGCCTGTGCGCTCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAGAGATCCAGGAAACTGTAGCTCTCTAGCTAGTGTCACTTAACTTAATGC
AATCAGGAAAGTAGCAAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
 GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
 AAGCCAGACTTCCCCAAATTCCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
 GTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
 AACATTTCATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
 GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
 TCCCAACGAGTTCTCAGGATTAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
 CTGACTGCATTTTGTCTTTTAGAAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
 ATGGAGAGGAA

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FIGURE 101

MAVLVLRRLTVVLGLLVFLTCYADDPDKPDDKPDDSGKDPKPDFFKFLSLLGTEIENAVE
FILRSMRSTGFMEFDDNEGKHSSK

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GGATGCCAGCGCCTGCAGAGGCTGAGCAGGGA AAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCC **ATG**GACATCCTGGTCCC ACTCCTGCAGCTGCTGGTGTCTTCTTAC
CCTGCCCCTGACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCGTGTG CAAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACTTTCA GTTCTACCCACCGGGCTGCAGGGTCACTGCGCTAGACC
CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGTCTGTCTCTGTGCAGAGCCCAAGGAAGTCTTCGAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCCACTGGAAACACATTTGGGGATGGTG
TGCTCTACCCAGAGACAGCTGGAAGGACTTGTAGAACGCCCACTGTCTCCGAAATCCAAATGG
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACC **TAG**CAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
CCGCCTTCGACAGTGA AAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTCTCCATGTTGTCT
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGA **ACT**GGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCCTCT
CTCCCCACTACCACTTCTTCTGAGCTGGGGGCCACAGGGAGAATCAGAGATGCTGGGGAT
GCCAGACGAAGACTCAAAGAGGCAGAGGTTTTGTCTCAAATATTTTTTAATAAATAGACGA
AACCAGC

FIGURE 103

MDILVPLLQLLVLLLTPLPLHMLLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDEVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFM
WQQVFEPETWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLFPVGPHIMGKAVKQSFP
SSKALICSFPPSLQLEQATHQPIYPLRGT

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CTGGGATTTATTATTGAGTGAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
TCCTGGCTGTGTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCCCAACCTATAGACTTTGTCCCAA
TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCGTGTGGTCATCGCTGCATCTG
AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTCAGCACAACTCGCTCCAAT
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATTCTCCGGTCTGGCTCAACAG
TGATTCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAA
AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACTTTTGAAGGTTCTAC
TTGCCAATTTCTGGTTCCTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
AGGTGATATCTTGCCCTTCTACAATACAGCATGAAGCGAGGACATGCAGCTGCATTTTCAG
AAGATTGTGATTACGCCCTCTACTAAAGTTGTGCTACCGTGGAGCGAGGAACCACTACAATTAC
ATTGGCTATCTTGACTATAAAAAGGAAAGAAATTCGTAAGCTTTCCATGAAGCCAGCACTTG
CTCATTTAATCCTGGAGTTTTTTGTTGCAAACCTGACGGAATGGAACGACAGAAATAACTA
ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCCTGGCT
GGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
TATGTGGAATGTCGCCACCTTGGTTCCAGTGCTGGA AAACGATATTCACCTCAGTTTGTA
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
ACTGATGTTTGGGAAAATGGTATATTCAGACCCAACAGGCAAATTCACCTAATCCGAAG
ATATACCGAGATCTCAACATATAAGTGAACAGAAATTTGAATGTAAGCAAGCATTTCTCAG
GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCATACGGTA
GCAAGCCATGGA AAAAGATGTGTGAGCTAGGTAAAGATGACAAACTGCCCTGTCTGGCAGTC
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTCTT
ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTTACGCTAGCTGGTACAGA
TAATTCAAAACCTGCTGTTGGTTTTAATTTTGAACCTGTGGCCTGATCTGTAATAAAACTT
ACATTTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIOHNTRSNIIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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TGGTTTTTGGCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTCTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCTCGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAAATTGTCAATTTTGACCTTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATTTCTTGCCTTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGCGTAGTGGGCGTGCGCGGCTGCCACG
 GAGTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGGCGCGGCGAGCCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGCCATTGCAGCTATAA
 ACAGCATTTCAGACAACACATCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATTCTCGGTCCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCCAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAAGAGATTGTGATTGAGCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC
 CTGACGGAATGGAAACGACAGAATATAACTAACCAACTGGAATAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGGAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGTATATTCCA
 GACCCAACAGGCAAATTAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAA
 CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAATAAGATGTGTGAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTGAGCTAGCTGGTACAGATAATTCAAACTGCTGTGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGGTAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCTGCTGTCATGGGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCTGAGAAGGCCCCACCACCCAGAACCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCCAGAGTCTAGCCAGCTTGCTCCAAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGTCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGGCCCCCTCCCTGGTCTCTCCAGTGTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGFWPSLEPRT

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STTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCCTCCAAGCAAGTCATTTCCCTTATTTAACCAGATGTGTCCCTCAAACACCTGAGTGC
 CTCCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCCTAAGTGGAA
 TCA**TGT**CGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATACCACCCTTCTGGTTACATTTTCATTTTCATTGGTTAT
 TTTGGGATTTGTTTGTCTGCGGTGTTTTATGTGGTCTATTATGACTATACCAACGACC
 TCAGCATAGAAATTCGACACAGAAAGGAAAAATATGAAGTGCCTGCTGGGGTTTGCATCTGTA
 TCCACAGGCATACCGGAGTGCCTGCTGCTTGATTTTTGTTCTCAGAAAGAGTAATAAAATT
 GACAGTTGAGCTTTTCCAATCACAATAAAGCCATCAGCAGTGTCTCCCTTCCTGCTGTTC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAACTGCAGGAGCTGCCAGGTTATGGAAGCGGCCAAGTGAATATAAGCCCTT
 TTCGGGCATTTCGTACATGTGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTC
 TCCTTGCGTGCCAGCAATGACTATAGCTGGGGCAGTGGTTACTTGTATTTCACAGAAAT
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGCTCTCTCTCCATTCTCTTCTTACCATCA
 AGGAACCGTTGTGAAGAGGGTCATTTTAACTCTGTGGTGAGGATTCGAGAATCATTGTCA
 TGTACATGCAAAAGCAGCTGAAAGACAGCAGCATGTGGTATGCTCAGGACTTACCTGTTCCGA
 TGCTGCTACTGCTGTTTTCGTGTCTTACCAATACTGCTCCATCTCAACCAGATGTCATA
 TACTACAACCTGCTATTAAATGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAACCTGCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGAGTCCCTCTGTTATTGGTAGCTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTGTCTGTGAT
 CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCAGCAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACGAACCTCAGGCCATTGTGAGATAGATACCCATTAGGATATCTGTACCT
 GTGAAACATTTTCTCTTAAGAGCCATTTCAGATAAGAGATGAGACCCTAGAGCAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAACCCATATTTCTCTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFIAIVSTGITAVLLVLI FVLRRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDFPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYT TTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

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FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGTTCTTGGACCTCTCCCTGTTTCTTCTCCTT
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAGCCCTAAGGGAAGAAAGATATTCATTCTGT
 TGTGGTGAATAATTTTGAAGAAAAAATTCCTTCAAAACAGGGGTGCATCTGTGATATT
TATGAGGACTGTTGTTCTCATTATGAAGGCATCTGTTATTGAAATGTTCTGTTGTTGCTGG
 TGACTGGAGTACATTTCAAACAAGAAACGGCAAAGATTAAAGAGGCCCAAGTTCATCTGTG
 CCTCAGATCAACTGCGATGTCAAAGCCGGAAGATCATGCATCTGAGTTTCATTTGTGAATG
 TCCAGCAGGATGCCAAGACCCAAATACCATGTTATGGCACTGACGTGTATGCATCCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTGATATTCAGGAGGGAATACTT
 GTTCGGAAGGTTGCTGGACACTCTGGTTACAAAGGGAGTTATTCAGCGGTGCCAATCCTT
 ATCCCTACCAGATGGAGAGAACTCTTTATCTCTTGAAGATAAACCCAAAAAGGGTGTA
 CCTACCCATCAGCTCTTACATACTCATCATCGAAAGTCCAGCTGCCCAAGCAGGTGAGACC
 ACAAAGCCTATCAGAGGCCACCTATTCCAGGGCACTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCAGCCCACTGCACAGCCGGTCACTCTGATGCA
 CTGCTTCTACCACCAGCATCCCCAGACCAATCAGTGGGCCACAGGAGCCAGGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCAGAGTGCATCCAGGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAACTGTTGGAGCGGATGTCAGCTGGGAC
 TTGTTCCAAAAGAAGATTGAGCACACAGTCTTTGAGCCAGTATCCTGGGAGATCCAAAC
 TGCAAAATTGACTTGTGCTTTTAAATGATGGGAGCACCAGCATTTGGCAAGCGCGATTCCG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTCATTTGGCCCTGCCGGTCCAC
 TGATGGGTGTTGTCCAGTATGGAGACAACCTTGCTACTCTTAACTCAAGACACACAG
 AATTTCTGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTCCGGCCATCTCCTTTGTGACCAAGAACTCTTTTCCAAAGCCATGGAAACAGAAAGCG
 GGGCTCCCAATGTGGTGGTGTGATGGTGGATGGCTGGCCCAAGCAAGTGGAGGAGGCT
 TCAAGACTTGCAGAGAGTCAAGGAATCAACATTTTCTTATCACCATTGAAGGIGTCTGTA
 AAATGAGAAGCAGTATGTGGTGGAGCCAACTTTGCAAAACAGGCCGTGTGCAAAACAAACG
 GCTTCTACTCGTCCAGTGCAGAGCTGGTTTGGCTTCCACAGACCTTGACGCTCTGGTG
 AAGCGGGTCTGCGACACTGACCGCTGGCCTGCAGCAAGACCTCTTCACTCGCTGCAT
 TGGCTTCGTATCGACGGCTCCAGCAGTGTGGGGACGGCACTTCCGCCCTCTCCAGT
 TTGTGACCAACTCACCAAGAGTTTGAGATTTCCGACACGGACACCGCATCGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTCCGACAAAGTACAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAATGGTGGCACCAGCAGCGGGGCTGCCATCA
 ACTTCGCCCTGGAGAGCTCTTCAAGAAGTCCAAGCCCCAACAGAGGAAGTATGATCTCTC
 ATCACCAGCGGAGGTCTTACGACGACGTCCGATCCGACCTGGCTGCCCATCTGAAGG
 AGTGATCACTTATCGATAGGCGTTGCCTGGGCTGCCAAGAGGAGCTAGAAAGTCAATTGCCA
 CTCACCCCGCAGAGACACTCTTCTTTTGGAGCAGTTTGCAACCTTCATCATGATGTC
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCACTCACAGCTCCGGAAC**TGA**ATTCCAGAG
 CAGGCAGCACCAGCAAGTGTGCTTTACTAATGACGTGTGGACACCCACCGCTTA
 TGGGCGCAGCCAGGTGCATCAAGTCTTGGGCGAGGCATGGAGAAACAAATGCTCTTGTATTATTA
 TTTCTTTGCCATCATGCTCTTTTCAATATTCAAAACCTTTGAGTTACAAAGATGATCAACAACT
 ATAGAATGAGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGAATTT
 GTTTTCAAAATGTTTGGAAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTTAAGTTGTTATTCTGATTTGAACCTCTGTAACCTCAGCAAGTTTCATTTT
 GTCATGACAAATGTAGGAATTTGCTGAATTAATGTTTGAAGGATGAAATAAAAAA
 AA
 AA

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVKAGKIIDPEFIVKC
PAGCQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQMDLWSTATYTTSSQNRPRADPGIQ
RQDPGSAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATFNKTHTN SRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKT LQPLVKRVC DTRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKFEISD TDTRIGAVQYTYEQRLEFGFDKYSSKPD I
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEF DN LHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
AGCCTTTCCGGCTGCTCATCCGCTCGGCCTCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGAATGTCTCAGAATTCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGCTGGGGTGGAAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGGCCGAAAACCTCC
 TCCCAGCCTTTAGACCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG
 AACCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGAACACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCGAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAG
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTGAGATGTACAGGGGACT
 GTGTCCATGCCAGTCTTCAGTCTTGGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGCGGGGATCCCACCTG
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTCTTCCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGTACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGTGGAGGACTTGATGAGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAAACTGTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAAACATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGTCCCA
 CTCTCAGCTGCCCCAGTCAGCCCTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCCT
 AGACTCCTCATAAACCATGGATAATTTTTTATTTTTATTTTTTGGAGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNULLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVFSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCGCGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGAGTCTACCA
AAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA
 AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATAACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTTGCGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
 CATTGCTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCCTGTTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTGTCGCCACTGTTGCTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
 TGGTCCTCCAGACACCTTGAAAAATAACCAATTACCCCGAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCATAGGTTTGCAGAAGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTCCGCCACGACAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGTTGGTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTIONCATCCCTTCGGTCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTAG
 TGTTCCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCACTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGGTGACAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACAGAGAATGCAGAAGTCAGTAACATGTGCATGTTGTTGTGCTCCTTTTTTC
 TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

MQTFMTVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNL SVLSTNMKHLMLMWSPVIA PGE
TVYYSVVEYQGEYESLTYSHIWTPSSWSCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS AW
SILKHFPNRRNSTILTRPGMEITLTKDGFHLVIEDLPGQFEFLVAYWRREP GAEHHVGMKVRSG
GIPVHLETPMEGAAVCVKAQTFVKAIGRYSAFSQTECVVEQGEAIPCLVLALFAFVGMFLILV
VVPFLVWMGRLLQYSCCPVVVLPTLKITNSQKLISCRREEEDVATLVAPEEELLR AWIS

Signal peptide:

amino acids 1-29

amino acids 230-255

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGAGGGGGCGAACCCCTTCGCGCGCAAGGG
GTTNGCGAACCCCTTCGCGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCC**ATG**TGGCGGCGACGGTGGCAGCGGCGTG
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
TCAACATCCGGGGCAAACCTGGTGTCGTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGGCGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACCAAGTTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCGCACCTACAGTGTCTCATTTCCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
TGGTAGGGGCTTGGGACCCAACCTGTGTCAGTGGAGGAGGTGAGACCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTAT**TAA**CCACCGCGTCTCCTCCTCCACCA
CCTCATCCGCCCCACCTGTGTGGGCTGACCAATGCAAACTCAAATGGTGCTTCAAAGGGAG
AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATCTTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAG
AGCTCTTGACCAAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAATGTGTGGCAAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTTTTTGATATAAAACCAAAAAATAACTTGTATCAAT
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTAGTTGTT
GTTATTTCCCTCTGTATTATTTCTTCATTACAAAAGAAATGCAAGTTCATTGTACAATCCA
AACAAATACCTCACGATATAAAATAAAATGAAAGTATCCTCCTCAAAAA

120/330

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKEPTWNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

09989279-111901

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TGCGCCTGGGGAGGCTGTGTGCGCCGGGAGCTCGGGGGTGTCTGGGGGCCGGGGCCGCCCTCTCT
 CGGAGTTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCCATCGGAGGGCTCAGCTACGTTTCAGGGGTGCACCAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTGAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCTGTAGCATTGGCCTCTGCCAAAGGTGACCGGTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCGGGGGACCCCTGTCTCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGACCAGCTCCAATACAACCAGCAGTTCTCTGTCTGCCATG
 ACCCCATCAACATCCAGTTTCACTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTTGCCCAACCCCTGTACCATTGCCTGGGTTCCTGTCGAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCCCTCATCTGGCCCTCTCCCATCTTCAATGGC
 AAGAAGGCATCGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGAT
 GTTCTGTGACATCTGAACAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTTCATTGTCTGGGTCCCTTGCACCTCCAGAGTTGATCTCGAGCCATCATCAACAGATAAAT
 ATGAAGGACCTGGTGGTGTCTTATGGAACACAGAGAACAGTCCCGTGACATTTCGCGCACTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATTATGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCTGCAATTGCGCTGAAGGACGGGGAGGAGACCAGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTACAAACTACCCCTCACCATTTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTCAAACTGT**TGA**ATAAAGCAGCAGGCCCTGCTGGCCCGGTTGGCTT
 GACTCTCTCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCAGCCAGTTTC
 TGAGAGCAGCATCAAACTGTCAAGGAATTGACTGAACGAACATAAGAGTCTCTGGATGGGTC
 CGGGAACCTGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCTGT
 TCCATCCCCCAGATCCCCCTGTCTGTCTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

0909079.11901

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKGCKALVFVKQFKTQQY
 YNVLKQICFEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDVVAAAGSTRQHLDLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRRERTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSFPVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGGENIYPAELEDFHHTHPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCCTGACATTTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

GAGCAGGACGCGAGGC**ATG**GACCCCGCCAGGAAGCAGGTGCCCAGGCCATGATCTGGACTGC
AGGCTGGCTGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCCGGGC
GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGCG
AGTGGGGGTTGCGGTTGGGACTCCCCGCGAAGAAATGACGCGGCGCTGGATCTTACGGG
TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG
CTACAGCTGTGTGGGCGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGCTCGTGAGCT
GCTACAACGCCAGCGATCATGTCTACAAGGGTGCTTCGACGGCAACGTACCTTGACGGCA
GCTAATGTGACTGTGCTTCTGCTGCTGTCGCGGGCTGCTGCTCAGGATGAATTCTGCACTCGGA
TGGAGTAACAGGCCCCAGGTTCTACGCTCTGAGTGGTCTGTTCGCCAGGGGTCCGCTGTAACT
TGACTCTCCGAACAGAGCTACTTCTCCCTCGAATCCCACCCCTGTGTCGGGTGCCCCCT
CCAGAGCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
ACCCACATCCACCACCAACCACATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAG
AACACGAGGCCCTCCGGGATGAGGAGGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAG
CGCAGCAATTGAGGCGAGTATCTGCAAAAGGGGGGCCCAGCAGCCCCATAATAAAGGCTG
TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
CATCACTTCTGTTCCACCACTGGACTGGGCTGGCCAGCCCCGTGTTTTTCCAACATTCCC
CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGGCGGCTTGGGAAATAAAATACCGTTGTATAT
ATTCTGCCAGGGGTGTTCTAGCTTTTTTGAGGACAGCTCCTGTATCCTTCTATCCTTGTCTC
TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTG
AGAGAGAGGATGCTAAGCTTCTACTCACTTCTCTCCTAGCCAGCCTGGACTTTGGAGCGTG
GGTGGGTGGGACAATGGCTCCCCACTTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
GAATCGGTTCCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGGCCGGTAC
CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 126

CGGGACTCGCGGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGTGTGCAGACGCC**ATG**GAGT
TGGTGCTGGTCTTCTCTGCAGCCTGCTGGCCCCATGGTCTGGCCAGTGCAGCTGAAAAG
GAGAAGGAAATGGACCTTTTCATTATGATTACAGACCCCTGAGGATTGGGGGACTGGTGTT
CGCTGTGTGCTCTTCTCTCGGTTGGGATCCTCTTATCCTAAGTCGCAAGTGCAAGTGCAGTT
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCAGGTGGAGAACCTCATCACCGC
AATGCAACAGAGCCCCAGAAGCAGAGAAC**TGA**AGTGCAGCCATCAGGTGGAAGCCTCTGGAA
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAAATGTCGATGCT**TAA**AAAAACCGGCACCTT
AGCAACAGCCCTTTCCCCAGGAGAAGCAAACTTGTGTGTCCTCCCCACCTATCCCCCTA
ACACCATTCCTCCACCTGATGATGACAACTAACACTTGCCCTCCCCTAGCCAGCTCGGGTCTCT
GCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTTGTCTAACTGTG
GTCTTTGTGGCTACTTGTTTGTGGATGGTATTGTGTTTGTGTAGTGAACGTGGAGCTCGCTTT
CCCAGGCAGGGGCTGAGCCACATGGCCATCTGCTCTCTCTGCCCCGTGGCCCTCCATCAC
CTTCTGCTCTAGGAGGCTGCTTGTGTCGAGACAGCCCCCTCCCCTGATTAGGGATGC
TAGGGTAAGAGCACGGGAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCAC
TTTGTATCATTTCTTCATGGACTCCTTTCACCTCGTTTAAACAAAAACCTTGCTTCCTTATCCC
ACCTGATCCCAGTCTGAAGGTCTCTTAGCAACTGGAGATCAAAAGCAAGGAGCTGGTGAGCC
CAGCGTTGAGCTCAGGACGGCTATGCCCTTCGGTGGTTAACTTTCTCCAGGGGCTTCCACG
AGGAGTCCCTATCTGCCCCGCCCTT**CAC**AGAGCGCCAGGGGATTCAGAGCCCGAGGCTTCT
ACTCTGCCCTGGGGAATGTGTCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG
GACCC**TAC**CCCTTCCAACTCTCCCTGCTCTGAGACTTCAATCTACAGCAGGCTCATCCAG
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCC
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGCCCTTGTCTTCTGCCTACG
TCCCTT**TA**GATGGGCAGAGAGGCAACTCCCGCATCTTTGCTCTGCCTGTGCGGTGGTCAGA
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAG
GTTGAAGGTACAACAGAGATGGGA**ACTCA**ACCAGACTCCCGCTTCTCTGTATCGTGATCTAT
CCCGCGAAACCAACCAACCTGCGCTGTGACCATTCCTGCTTCTCTGTATCGTGATCTAT
CTCTCAACAAACACAGAAAAAGGAATAAAATATCTTTGTTTCTCT

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDDEEAQVENLITANATEPQKQRTEVQPSGGSLWNLRRLLEPLDANVDA

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FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE
FLNWHALFESIKRKLPFLNWDAFPCLKGLRSATPDAQ

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CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGCGGGGTGGAGATTGC
CTTTGCCCTCAGTGATTCTCACCTGCCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTC
TTCCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGCGCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCACCCCTCA
AATTTTTGTATTACTAGATGGCTTCCATTTACCCACCACTATTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTGACTTGAGAAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATTATC
TTCACATATTAATTGTAACGATTAAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAAATATT
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTATTAACATAACCAATCTATTCTT
AAAAGTTTTGAGTATATTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTAGTG

.....

FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

THE

GGGGAATCTCGAGTAGGTCTGCCGGCGA**ATG**AGAGTGGTGGGCTAGCTCGCCGCTTCGGGCTCTGCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGAAGATATTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAACATGCAGCTGCTACCATGGTGT CATAGAAGAGGATCTAACTCCTTTCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCTACTAAGAACA GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT TTGGAAGTGATCGGGCGTCTCCTTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA GGTTCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTACGCAGCACAGTG GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG ATCCTCTCATCTTCTGTCTCGGAAAAACCCAAAACCTTGTGTGATGCAGAATACACCAAAAAC CAGGGCTGGAAATCTATGAAGAATACCTTAGGAAAGCAGCTGTCTAAGGATGTCCATCTTGT GGATCACTGCAAAATACAAGTATGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTA AACACCTCTTCTGTGTGGCTACCTGTGTTTCCATGTTGGTGATGAGTGGCTAGAAATCTTTC TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAAGTCAAAACAGATCTCTCCAATGTCCA AGAGCTGTTACAATTTGTAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG AGTGAATACTCTAAATTCCTGTCTTATAATGTAAACGAGAAGGAAAGGTTATGATCAAATTA TCCCAAAATGTTGAAACTGAACTA**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA TCTGCTATCAAGCCAATACCTGGTTTTCTTATCATGCTGCACCAGAGCAACTCTTGAGA AAGATTTAAATGTGTCTAATACACGTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA CCAGAAATCGTGAGATGTGGATTTTGAACCCAACCTCTACCTTTCATTTTCTTAAGACCAAT ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAAATTCGTCATTTGGAAGTAGTACAA CTCATTGCTGGAATTGTGAAATTATTCAGGCGGTGATCTCTGTCACTTTATTTTAAATGTAGG AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATTTCTCTGAATGGTCTAAGGAAGCGG TAGCCATGCCATGCAATGTAGGAGTCTCTTTTGTAAAAACATAAACTCTGTACTACAGG GAGGTTTCTATAATGCCACATAGAAGAGGCCAATTCGATAGTAATATTATGCAATTGGATT TCAGGTTCCCTTTTTGTGGCTTTCATGCCCTACTTCTTAAATGGCTCTCTAAAGCGAAA

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MEWASSPLRLWLLFLPPSAQGRQKESGSKWKVFIQINRSLNENYPCSSQNCSCYHGVE  
EDLTPFRGGISRKMMAEVVRRLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD  
MEMVINVRDPQVPKWMPEAIPVFSFKTSEYHIDIMYPAWTFWEGGPAVWPYIPTGLGRWDL  
FREDLVRSAAQWPWKKNSTAYFRGSRTPERDPLILLSRKNPKLVDAEYTKNAWKSMDKT  
LGKPAAKDVHLVDHCKYKYLNFNRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPVVH  
YIPVKTDLNSNQVELLQFVKANDDDVAQIEAERGSQFIRNHLQMDITCYWENLLSEYSKFLSY  
NVTRRKGSDYOIIPKMLKTEL
```

FIGURE 134

CACCCCTCCATTCTCGCCATGGCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGTATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCCTAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCTCTACCTGGGCCTGGCTACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGGCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCAGTGTTCAGCCA
 CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCCTGGCACTGTTACTTGCCCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCAATAGCTGTCCCTCCA
 GGCCCCAACCTTGCCCTCACCACCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAAALASFILAFGTGVEFVRFTSLRPLLGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVVPTLGTDRLLLAFLTLTYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGACAGGAGGATTGCCTCGCTTTTAGGAGGTGGCTGCGTTTGGGAAAAGCTATCAAGGA
AGAAATTGCCAACCATGTCTTTTTTCTGTTTTCAGAGTAGTTTCAACAGATCTGAGTGT
TTTAATTAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAAGCTTTAATTTTCATCTGGAATT
CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
TCACGTGCTGCTCTCCGACTACTACCCCGAGTGTAAGAAGCTTTCGGCTCGCGTGCTCTCG
AGCTGCTGTGGATGGCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCTACTGAGATCC
CTCAAATGGAGCCTCCTGCTGCTGCTACTCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
TCCCCACTACAATGTGATAGAAGCGGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
ACAGACAAGACTTTCACTTCACTTCCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
CTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTTAGAGGATGAACACCTTCTTTATGGT
GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC
ATTCAAGTGGGTAACTGAGTTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
TTTTCTCAATCACTGCGCAATTTAGTGAAGTATCTTTAAACCTAABACCCTCAGACAGATTT
TTCACAGGTATTCCTCTAATTGATAATTATTCTTATGAGAGTATTACCAAAAAACCCATAT
TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA
TGTCAGAGATTGTTGCCAAGGATCTATGAAATGATGGGTACGTAAGAACCCATCAAGTTT
GAAGATGTTTATGTGGGATCTGTTTGAATTTATTTAAAGTGAACATTCATATTCAGAAGA
CACAAATCTTTCTTTCTATATAGAATCCATTGGATGTCTGTCAACTGAGACGTGTGATTG
CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTGATGCTAAGGAACACC
ACATGCCATTATTAACCTTCACATTTCAAAAAAGCCTAGAAGGACAGGATACCTTGTGAAA
GTGTTAAATAAAGTAGGTACTGTGAAAAATTATGGGGAGGTGAGTGTCTGGCTTACACTG
AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTC
AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTGCTAAA
GAAATTAATAGGACCAACAATTGGACATGTCACTTCTGTAGACTAGAATTTCTTAAAGGG
TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG
AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
TGTAAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
TGGTCATTTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
CATCTTTTACATGCAACATTTTCCAGTTACTTAAGTACGATCAGTTATTATTATGATACATCA
TCCATTAATGTAAAGTCACTAGGTCATTATGCATATCAGTAATCTCTTGGACCTTTGTTAAAT
ATTTTACTGTGGTAATATAGAGAAGAAATTAAGCAAGAAAACTGAAAA

FIGURE 137

MASALWTVLPSRMSRLSLKWSLLLLLSLFFVMWYLSLPHYNVIERVNWMYFYEYEPYIRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTLTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLNLNHNSEKFFTGYPLIDNYSYRGFYQKTHISYQEYFPKFVFPYCSGLGYIMSRD
LVPRIYEMGHVKPIKFEDVYVIGICLNLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFVQWMLRNTCHY

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGACTAAACAATTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

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FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNFGAATRLFQKKTIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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FIGURE 140

CATTTCTGAAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTTGTATATGCTAGAAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAAATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCGGTTGCCAACTCGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCGAAGAAAAAGCCAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTAAGCAAGGGA
 TTGAATCCGGATGGAAGTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAGAAAA
 GACAGCAAGAGAAGTAGAATATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCTTGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAACGCAAACCTGATTAGGATTTGATTCTTGAAACCCCTCA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAGAAGTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAAGAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACITGGAGCGTGAATCTGTAAAAATGTATCTTATTTT
 ATACAGATAAAATTCAGACACTGTTCTATTAAAGTGGTTATTTGTTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGATTTTTACAGGAAATAAAATACAAAT
 CTGTTTTTTCTAAAAAAGGAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKSRSRSQ
SKSRDHS DAAKKRHERGHRDRRERSRSFERSHKSKHHGGSRSGHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTACAGAAATATAT
TANCTTTTtagagTAATTTCTAGTTGGATTGTAATATGAAATTATTTAAAAGGCCTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAGTAGAAAAAGAAAAGTAGCCTTACAAGAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAACTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

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REF: 620800

FIGURE 143

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGT**CATG**GC
 GGTCTCGGAGTACAGCTGGTGGTGACCCGTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
 CAACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAAGACGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCACTGG
 TTTGTGGACTTTGCTGTGTACTCGGGCGCGTGTACCTCTTACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCAGCGTGACCTTCT
 CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCTTCTCTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
 GGAGGAGACCTCGAGCTGGGCCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCCTGCGGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCCTGCG
 ACACCAGCTTCTGTCTCCCTGTTTCATCTGTGGCTCTGGACAAAGCCCATTCGACGGGAC
 TTCCTGCACACGCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGCTGTGCTGCGGCTGGCGGTGACCCGCCCC
 ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCGGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCCTGCTTACTCCCTCTTCTCCGTGGCGTCTGGCCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTTACTTCCACCAGCACTTGGCA
 GGCTCCT**TAG**CTGCCTGCAGACCTTCCTGGGGCCCTGAGGTCTGTTCTTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGGCGCCCCGTGTCCCAGCTGCAAGTGGGGCCGGACTCCCC
 GGCGTTCCCTTACCACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
 GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGTAGTGGCGAGGGTGTGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTAA

 068279 11931
 TGGTTG 52855

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSABEEGERSVCLTFAFLFLLAMLVQV
VREETLELGLPEGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRMLQFLLHTSFLSPLFILWLTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLQYLTPLIILTLCNTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSEDEVQQTAAARI
AGALGGLLTPFLRGVLAYLIWWTAAQQLLASLFGLYFHQHLA

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FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGC
TTCTTCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCTGCTGCTGGC
CATGCTGGTGCAAGCG

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FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAACTTCTTACGGGCGCGTGATTATTAACTGGCCTT
 AATCTGAAGGTTCTCAGTCAAATCTTTGTGATCTATGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTTAGCTGACAGAAGTGGCCAGGAGAAATCAGCACACTGCTCGGAGAAAGG
 CGCTTCTGTGCTGGTCTTGGCCTTGGCTCAGTCTTGCTAACTACATTGACAAATGTGGGCAACCTGCACCTTCTG
 TATTCAAGAACTCTTAAAGGTGCCTCCCACTACGGCCTGACCAAGATAGGAAGAGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTCCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGTTTCTCGAGCTGCCACCATCTCCTTAA
 TGCACAGCAGCCTGGCCTTAGACAACCTGCCTACGTGTCTCTCGGAGAGGACGGGACGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAAAATAATCGAGCTTTGAGTGTCTTTCGAAGGACAAAGACGGGGATGCAAGTTGCCAACCATGCCGACGAGG
 GCAGGAAAAATCTGAAAACACCACTGCCCCCTGAAGTCTTTCCAAGTTGTACCACTGATTCCAGATGGTGAA
 ATTACGAGCATCAAGATCAATCGAGTAGATCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAAACATTTATCGTGATGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTCAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACTACGCTGTGCTCTCTCGGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAAACAGAAGTTCCGAGCAGGAACATGGACAGGCCCC
 GGATGCCTACAGACCCCGAGATGACAGCTTTTATGTGATTCTCAACAAAATAGCCCCGAGGAGCAGCTTGGAA
 TAAAACTGGTGGCAAGGTGGATGAGCCTGGGGTTTTATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAAGGAAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCGAAG
 TCGGGCTCATCTGATTACAGGCCAGTGAAGAGCTGTTCACTCGTGTGCTCCCGCAGGTTGGCGAGCGGAGCC
 CTGACATCTTTAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGAGAGGAGCAACACT
 CCCAAGCCCCCTCCATCTCAATTAATCTTGTATGAGAAGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGCTCGCAGGGGAGCATCACATAGAGAATGGGATTTGCTTATCTATGTGATCAGTGTGTAGCCCG
 GAGGAGTCATTAAGCAGAGATGGAAGAATAAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAATCTGACA
 GAGGTGAGCGGAGTGAGGAGCTGGCATTTATTGAAAAGAACATCATCTCGATAGTACTCAAGCTTTGGAAGT
 CAAAAGATGATGAGCCCGAGGAAGCTGCAGCAGCCAGCAGCCTGGACTCCAAACCAACATGGCCCAACCCA
 GTGACTGGTCCCCATCCTGGGTGATGTGGCTGGAATACCAAGGTGCTGTATTAATCTGTAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGATTTAGGAGGTTATGAAGAATCAATGGAACAAACCTTT
 TTTTATCAAAATCCATTGTTGAAGGAACACCGCATCAATGATGGAAGATTAAGTGTGGGATATTCTTCTTG
 CTGTCAATGCTAGAAGTACATCAGGAATGATACATGCTTGTGTCAGACTGCTGAAAGACTTAAGGAAGA
 ATTACTCTAACTATTGTTCTTGGCCTGGCACTTTTTATAGAAATCAATGATGGCTCAGAGAAAAACAGAAAA
 TCACAAATAGGCTAAGAAGTTGAAACACTATATTATCTTGTCACTTTTATATTTAAAGAAAGAAATACATTGT
 AAAAATGTGAGGAAAAATGATCATCTAATGAAGACAGTTCACACCTCAGAAAAATGATTGTTCCAAAAAATTA
 AAATCTAGTTTTTTTTTTCAGTGTGGAGGATTTCTCATTAACCTACAACTGTTTATATTTTTCTATTCAAT
 AAAAAGCCCTTAAACAACTAAAAATGATTGATTTGTATACCCCACTGAATTCAGGCTGATTTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCAAGGTTACATATGGCCATTTTATTTACAGTCAAAATATTTTTTAAATATGCA
 TTGCTGAGAAACCTTGCTTTTATCAAAACAGAATAAATATTTTTCAGAAAGTTAAA

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MKALLLLVLPWLSPAYNIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
 APSPEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
 FKINRALSVLRTKSGSAVANHADQGRESENTAPEVFPRLYHLIPDGEITSIKINRVD
 SESLSIRLVGGSETPLVHIIQHIYRDGVIARDGRLLPGDIILKVNMGDISNVPHNYAVRL
 RQPCQVLWLTVMREQFKFRSRNNGQAPDAYRPRDSDSHVILNKSSPEEQLGIKLVRKVD
 EPGVFI FNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERFVHLVVS
 RQVRQRS PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNIQKDPGESLGMT
 VAGGASHRE WDLPIYVISVEPGGVISRDRIGTKGIDILLNVGVELTEVSRSEAVALLKRT
 SSSIVLKALEV KEYEPQEDCSSPAALDSNHNMAPSDWSPSWMWLELPRCLYNCKDIVL
 RRNTAGSLGFCIV GGYEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMI
 HACLARLLKELKGRITLTIVNSWPGTFEL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCTCTCCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCTGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGTTTTACACTCAAAAGTCAAATTAAATTCTTTCCCAATGCCCAACTAATTTTGAGATTC
AGTCAGAAAAATATAAATGCTGTATTTATA

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FIGURE 149

MKILVAFLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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FIGURE 150

GGCACGAGCCAGGAAGTCTAGGAGGTTCTCACTGCCCCAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCTTACAAAGTCTTGGAAGTTTTCCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCTCCTT
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
 GATGATCTGCCAGGCGTCCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
 AGCCAGACATCGGACTGGTCTGCTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCCTGGAGA
 GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
 GGGTTCAGGATAGGGAATGGGGAGGTGAGAGACGCAAAGCAGCAGCCATGTAGAATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTTCGTATTTGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPPIITNSLIGKDGQVHLQQRPFCHRPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

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FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTTCAAGCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCTTGGGGAAGAAA
 CTAAATGTCACAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTCAGAGAGCACCCTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCTCATCTTTGCTGCCTCCTCATCTCCTCCCTGCTTCATCTCCTTGCCA
 TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGATGTCCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTATTCACTGCCTTGATTCCTT
 TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTCTTC
 TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGCTCTGAAAGAG
 AATTTTAAATTTATTAATAAGAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
 TGTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCCAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFE
HYDCGNKTVTPVSPGLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQPSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

GGGAAGCCATTTCGAAACCCATCTATACAACTATATATTTTCATTCTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTCTGACTTTCAGTTATATACCGTGGGAATGAGG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCAATTCTG
GTGTGGCTTCTTTTCAGAGGATTCCACCTTCAAATCATGAACCTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTAGGTGATGGCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTCCTCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT
CCTCTCTCCATTCAAGCATCAAGTATATTTTCAATGAATTAACCTTGACAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATTGCTTTTACCAATGAGAGAAAAAATGCAATTTCTGTAT
CATCCTTTTCAATAAACTGTATTCTATTTTGAAAAAATAAAAAAAAAAAAAAAAAA

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FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

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FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAAGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGCTCGTGCAGTAACCAAGTTACGAAGGTGGTGTGCACCGCCGG
 GGCCTCTCCGAGGTCCCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTCGAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTGCACAACTGGCTGACAGTCATCCCTAGCGGGGCTTTGAATACCTGTC
 CAAGCTCGGGAGCTCTGGCTTCGCAACAACCCATCGAAAGCATCCCCTCTTACGCCCTCA
 ACCGGGTGCCCTCCCCTCATCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTGGTGGGGCTGGAGAGCTGGAGATGTCAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTATG
 AACTCACAGGTGAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACTTGGCCCAATAAAGCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTGTGATCTACACCACAACCCCTTGGAACTGTGATTGTGACATCTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCAACCAATTCACCTGCTGTGGCCGCTGTCATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACAGGCCTCCTTCCAGTGCCTCTGCCCCCT
 TCATCATGGAGCACCTCGAGACCTCAACATTTCTGAGGGTGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGTCTAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGCTGCTGC
 TTTCAGACACTGGGGTGTACACATGTCATGGTGACCAATGTTGCAGGCAACTCCAACGCCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTA
 CCAGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGTCTATTACAGATACC
 CGTGTGCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT
 GGTGAAGTATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATGTCTTCTATAAACTTCGTAAGCGGCACACGACGCGGAGTACAGTC
 ACAGCCGCGCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGTTGATCAGGTGAGGGGGCAGTAGTGTGCCCACAATTC
 ATGACCATATTAACTACAACACCTACAACACGACATGGGGCCCACTGGACAGAAAACAGC
 CTGGGAACTCTCTGCACCCACAGTACCACCTATCTCTGAACCTTTATATAATTCAGACCA
 TACCAAGCAGAGGTACAGAACTCAAAT**TGA**CTCCCTCCCCAAAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
 TATGCTTATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGA
 CAAAAAGTCAAAACA

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FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLYLNLGMCNIKDMPNLTPLVGLLEELEMSGNHFEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLP HDLFTPLRYLVELHLHHNPWNCD CDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAE LNTSNYSFFT VTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATD TTDKMQTS LDEV MKTKIIIGCFVAVTLLAAAMLIVFYKLRRHQORS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLTPIHDHINYNTYKPAHGAHWTE
NSLGN SLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 158

CGCTCGGGCACCAGCCGCGGCAAGGATGAGCTGGGTGCTGGACGAGTTGGGGCTCACTTTTCTTCAGCTCC
 TTCTCATCTCTGCTCTGCCAAGAGAGTACACAGTCATTATGAAGCCTGCCTGGAGCAGAGTGGAAATATCATG
 TGTCCGGAGTGTCTGTAATATGATCAGATTGAGTGCCTCCGCCGGAAGAGGGAAGTCTGGGTTATACCAT
 CCCTTCTGCTCAGGAATGAGGAGATGAGTGTGACTCCTGCTGATCCACCCAGGTTGTACCATCTTTGAAACT
 CGAAGAGCTGCCGAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAG
 TGCCGAGCAGGCTGGTACGGAGGAGCTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGGTGAGTTTT
 GTTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGAACATTATGCTAAACCTGGGTTTGTGATCCAACATA
 GATTTGTGATGTGAGTCTGGAGTTGACTACATGTSCCAGTATGACTATGTTGAGGTTCTGATGGAGACAC
 CGCGATGGCCAGATCATCAAGCGTCTGTGTGGCAACGAGCGGCCGCTCTATCCAGAGCATAGGATCCTCACT
 CCACGTCTCTTCCACTCCGATGGCTCCAGAAATTTGACGGTTTCCATGCCATTATGAGGAGATCACAGCAT
 GCTPCTCATCCCTTGTTCATGACGGCAGCTGCGTCTTGAACAGGCTGGATCTTACAAGTGTGCTGCTTG
 GCAGGCTATACTGGGCGAGCGCTGTGAAAATCTCTTGAAGAAAGAACTGCTCAGACCTGGGGGCCAGTCAA
 TGGGTACAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGAGCCATGCTAAAATTTGGCACCCTGGTGTCTT
 TCTTTTGAACAACTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGGCAGCAGAATGGAGAGTGGTCAGGG
 AAAACGCCCATCTGCATAAAAGCCTGCCGAGAACCAGAAATTTACAGCCTGGTGAGAAGGAGAGTTCTCCGAT
 GCAGGTTCAAGTCAAGGGAGACACCATTAACAGCTATATACTAGCGGCCCTCAGCAAGCAGAAACTGCAGAGTG
 CCCCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG
 TATGATGTCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAGTGGAG
 TGGGCGGGCACCCTCTGCATCCTATCTGCGGGAATTTGAGAACATCACTGCTCCAAAGACCCAGGGTTGC
 GCTGGCCGTGGCAGGCGCATCTACAGGAGGACCAGCGGGTGCATGACGGCAGCTACACAAGGGAGCGTGG
 TTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTTACTGACTGGG
 GAAGGTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAATTTACACGGGATGATGACCGGGATG
 AGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTCTGCATCCCACTATGACCCCATCCTGCTGTATGCT
 GACATCGCCATCCTGAAGCTCTAGACAAGGCCGCTATCAGCACCCGAGTCCAGCCCATCTGCTCGCTCGAGCAG
 TCGGGATCTAGCACTTCTTCCAGGAGTCCACATCACTGTGGCTGGCTGGAATGTCTTGGCAGAGTGGAGGA
 GCCCTGGCTTCAAGAAGCACACTGCGCTCTGGGGTGGTCACTGTGGACTCGCTGCTGTGTGAGGAGCAG
 CATGAGGACCATGGCATCCAGTGAAGTGTCACTGATACATGTTCTGTGCCAGCTGGGAACCCATCGCCCTTC
 TGATATCTGCACTGCAGAGACAGGAGGCATCGCGGTGTGTTCTCCCGGAGCAGCATCTCTTGAGGACCAAGCT
 GGCATCTGATGGGACTGGTCACTGGAAGCTATGATAAAACATGCAGGCCACAGGCTCTCCACTGCTTCAACAG
 GTGCTGCCCTTTAAAGACTGGATTGAAAGAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAAGTGTTC
 TGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTTGGCCTGTGAACCTGG
 CTGTGCCAGGGCTCTTGACTTCAAGGACAAACCTGACTGCTGGTGTCTTCCCACTTCAAGTTATACGAATGCCATCACTTG
 GCCGCTCCACTACTAGGACGCCAATTTGGAAGTGCAGGCGCTGCAAGAAGTAAGTTTCTTCAAGAAGAACCC
 ATATACAAAACCTCTCCACTCCACTGACTGCTGGTGTCTTCCCACTTCAAGTTATACGAATGCCATCACTTG
 ACCAGGGAAGATCTGGGCTCATGAGGCCCTTTTGAAGCTCTCAAGTTATAGAGGTTGCTTGTGGGACAGCC
 CAGGGCAGCAGCTGGGATGTGTGCTGATGCTTTGAGGCTCTCAAGTTATAGAGGTTGCTTGTGGGACAGCC
 CATCTCTTGTACACATTTTAAATAAATAGGGTTGGCTTCTGAACTAACAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREV
GYTIFCCRNEENECDSCLIHGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDQIIKRVCGNERPAPIQSIGSSLHVLHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCEENLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILL
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSFGFKNLTLRSG
VVSVDVSLLEEQHEHDGIPVSVTDNMFCAWSEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMLVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK

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FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACAGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCACCTTTCCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGTGGGCCACCAGTAACACTTCGTGGGTGCCATTCAAGAGATTCTTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAAGTTGACAACGTCTCTTCTGTGTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCCAAGACGATGACCTCAGACTCAGGTTTGAGCTCCAAAG
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAATAATACAAATGGTCTTCCACACTAGAG
 ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCACGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGAATTTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTTGTTGAGCTGAATTTTTCCTTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGTATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAAGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGCTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCCGACGAATCA
 GGACACAGTGAAGTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAAATA
 TGTCTATCAAAATACCTCTGTAGTAAAAATGTAAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIVIHQAEGKKFNRAKLLNVGYLEALKEEN
WDCFIFHDVDLVPENDFNLYKÇEEHPKHLVVGRNSTGYRLRYSGYFGGVLTALSREQFFKVNG
FSNNYWGWWGGEDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 163

MAQAVWSRLGRILWLACLWPAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGF
VVLPITEFLVGDVLVVTQNTSLPWPSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIIGTFTVKLVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDEPD
YCFsIRAENIISKTHQYHKIQVWPSRIQPAVFAFPcATLITVMLAFIMYMTLRNATQQKDMV
ENPEFPsGVRCCcQCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

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FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

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FIGURE 166

CTGTCAAGGAGGACCATCTGAAGGCTGCAATTTGTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTCTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGCTCTTCCACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAAGTCTG
 GAGTCTTGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCCGGCTCAC
 GGTCTGTGGGGTTAGGAGTGCTGATTCCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGC
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCAGTCCATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACGGGGGACTCATGGGTGTGATTACAGAGCCATGGTGAAGGCTG
 CCCACACGTCTGGTTTGGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCAAGTTTACCC
 TGTGTCTATCAAGTATGACCTCAATTTGGCGATGCTTCTGGAACAGCAGCAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
 AAGGACAGGAGCGCTCCT**TGA**CGCTGCCTCCAGCTGGCTGGGGCCACCGTGGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTGTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGACGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTTTCTTTTACAATAAGTCTGTTGGAGGAATGCCATTAAAGTGAACCCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGGCGTACAAGAGTCTGTTATGAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG
 CTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCCGCTCAACATCGCCCCAGC
 CTGTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCACTCTGCAGGGGCTTTCAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGAGAACGTGTGTTCTGATCCAGGCTAACCCCTGAACCTCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGTGATTCTCACTCACAGGCTGTGTGGGGAATTAAGTGTCTGCGGTGAGTGA
 AGGACACATCAGTTTCAGTGTTCAGTACAGGCCCAAAAACGGGGCACGGCAGGCTGAG
 CTCAGAGCTGCTGACTGGGCTTTGGATTGTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

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FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFTIIVPAIFGVSFQIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAAELESWNLLSRTNYNFQYISLRLTVLWGLGVLRICYCFLPLRLALFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
TSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMFVKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

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GCCCTCGAAACCAGGACTCCAGACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
 CGTCTCCTCCAGGGATGCGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCAG
 ACCTGGCAGGCCAGGCTGTTCCACCATCTGCCCTGGGCTGGCTCCAGACACCTTTGA
 CGATACTATGTGGTGTGTCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCACCATGCCCTGCTGCGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGTT
 CTACACCAACTCATCGAACACCTTGTA CTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
 GCTCCCGGAGCTCTACATGAGGCACCTTCCCTTCAAAGCCCTGCATTCTTCTACCTGATCCGG
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGTTGTTCCG
 AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
 TTGCTCCAGCTCCCTGGATAAGGCAGTGGCCCACAGATTGGGGGAGAAGAGGCGGGGCTGT
 GTGTCTGCCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
 GAAGACTCTGCTCTTGGCCCCTGAGAGTTCCAGCTCTCAGGGGTTGGGCCCTGAAGATCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAAGCAAGAATCGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACAGG
 ATGTTGGCCTGAGGAGGCCACGAGGGCTGAGGAACCTGCTATGTGATGGGGACTTCCT
 GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPFKALHFYLIRALQLLRSGGCSRGPGEVVFRRVGSRLRFEPKRLGDSVRLGQFASS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLLLAPGEFQLSGVGP

GTGGCTTCATTTCAGTGGCTGACTTCCAGAGAGCAAT**ATG**CGTGGTTCGCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCGGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCAGGAGTACGTGCTGCATGCTTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTATACCTGGAAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCTGTCTCAGCAGAAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCTGTGTCTCCTGTTGGTGCCCTT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTGTCGGGAAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCAC
TGCTCAGCATGTCGCAGACACCAACAGGCTATTTCCTATGAGAATGTTATCT**TAG**ACAGCAGTG
CACTCCCTCAAGTCTTGCTCA

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFLPKSKVKQVDSIVWTFNTTPLVT
 IQPEGGTIIVTQNNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
 YEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSLPIPSWRW
 GESDMTFICVARNPVSRNFSSPLRLKRLCEGAADDPSSMVLCLLLVPLLLSLFVLGLFLW
 FLKRERQEYIEEKKRVDICRETNPICPHSGENETDYDTIPTHNRTILKEDPANTVYSTVEIP
 FKMMENPHSLLTMPDTPRLFAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
 TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTC
 CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
 AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
 GATGGAGGCTACTCCCTGAAGCTCAGCAAACGAAGAAGAATGACTCAGGGATCTACTATGT
 GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
 AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
 ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
 GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
 AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAGCAGAACTTCTCAAGCCCC
 ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCAGATTCTCCATGGTCTCTCT
 GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTTTC
 TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA
 ACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
 TAGAACATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA
 AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCGCTATGAG
 AATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCCTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGACTCCACCATCATCCCTTCTTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACCCCTTGACAAAT
TTTTTCATGAAATTATTCCTCTTCTGTTCAATAAATGATTACCTTGCACTTAA

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FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
 TGGATTTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
 TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTGCTTTGAGTGGTGGTTC
 CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
 AAAAAGAGCGTGCTGCAACAACAGAAGTGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
 CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGTCCCTCTC
 ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
 CATTCATCCAGAATCCTTCAACTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
 GTTTCATAAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
 TTCGATTCTGAAGAAAACAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT
 TGTGGAATTCTGGAGGTCCGTGTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
 TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
 TCAGTAGTTTGAAAAAAAAAAAA

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FIGURE 176

MTCCEGWTS CNGFSLLV LLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPNSNA
NCEFS LKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRL
IHFSVFLG LLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAA**TAG**TGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTCCAAAGTCTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKRRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGAC**ATG**GAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCCTTG
AAGCCAATGACCCATTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGC**TGA**GCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGLLAIAAGIAAVLSGKCK
YKSSQKQHSFPVEKAIPLITPGSATTC

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GAGGAAGAGGTTGTGTGGGACAAGCTGCTCCGCACAGAAGG**ATGT**CGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACTGCCGCCGGCTCC
 AGTGTTTCCACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCTATCGTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGACCCAAGGATAATCTCTTATCAGGTTCTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGAGCCGCCACCCTCGGATGCTGAC
 GCCCGCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCTGCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTTACAGAAATGCATCTTCACTTTGACAGCCATTG
 TCAGAGAGGGCCCACTGAATATATATGCCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAA
 GAAGCCAGCATATCTCCACAGACATGGACCTTCTGTAATTACCTTCTCCATGACGGCGGCGC
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTACAGACGCTGTCTATCCGGGAGCGGCTCG
 CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCAGAGCACCAGAATACCAGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCGATCTTAAAGAGATTGAATGGGACGACCTGCCCCAGCTGCC
 TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCACTCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCTCTGAGGTCTACGAC
 CCCCTTCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACTCTGGCTTTTATTCCTTTCTC
 CGCAGGGCCCAAGTCACTGTCAGCGGCACCGCTTCCGCTAGGCGAGATGAAAGTGGTCTGTG
 CGTTGATGCTGCTGACCTTCCGGTTCCTGCGGACACACATGAGCCCGCAGGAAGCTGGAA
 TTGATCATGCGCGCGGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATGTCTATGAATAAAACCGTGTCTCAAA

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTTCAGGATTCTTAAATCCTCTCTTATCTCTTCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGAGGAGCTAGAAA
GAGCTTCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACCCAGAGGAAATTTGAGAAAGTTTCAGGATT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCTGATTGCTTCTGAAATACTGTGTC**TGA**AGTGAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCTGTTCAATTGTTACCTGGAAATAAATCCTCT
ATGTTTTGCACAAAAA

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FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

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FIGURE 186

MPSPGTVCLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGTGTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGT
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTCTAACAAATGAAATATATTACAGGCAGGTCACCCCTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACAACCTCCCTGCTCTGGCACCAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAGCG
 TCTTCCATCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGCCA
 ACCCTTGTCAGGGCAGAGGGAGTTGGGTGGTTCAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAACCAAGA
 GCCTCCTTGTTTATAACCACAGGTTACCCTACAAACCACTGTCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDFLGLVHLGQLLIFHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAELTPRPAGVVPGA

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FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCGTGTGCGAGAAAGGTCTGGCAGCCAAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCTCTCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCCTCTGTCTGTCAAGTCTCCTGGGGATGGTGGCCACATGATGTATTCACAAGTC
 TTCCAAGCGACTGTCAACTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTG
 GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCAACCACCTTCA
 ACAGTACACCAGGATGGTGCTGGAGTTCAAGTGAAGCATTAGTAAAGAGCTTCAAGGAAAAAC
 CCGAAGTGCCTACCACATCACCATCAGTGTTCCTTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCCTTTGACCAGCTACCACAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGCTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTCTCTACAGCTCCATCTGTGTTTCAACCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGTNTSTQEYVQYNWETGDDRFSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPGCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQ
PPATNRLATHWEFCLWAQTERLCCCFLCPVRS PGDGGPHDVFTSLPSDCQLGSRRL ETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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AACCTGGAAGGAAAGAAAGAAAGGTACAGCTTTGGCCCA**GATG**TGGTTACCCCTTGGTCTCTGTG
TCTTTATGTCTTTCTCCTCTTCTTATTCTGTCACTCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGACCCTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCTCTCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGTCAGCCAGTATTAACATGTCCTCTCCCTTCCCCCTGCCCGCGGTAGATTAG
GACATTGCCCCCTGTGTGCCACCAAAACAGGACTTCTCCCTTGGCTTGGCATCCTTGGCTCT
CTCCTGGTACCCAGCAAGACGCTCTGTTCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCCTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTTGAGGAAAAACAAA
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTTATCGGAAAGATCATCTTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGAAGGAA
ATAGAACAGTCTGCTGGAGTGCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGG
AAGTCACTCAGCTCCCGAGTACGACCTCTCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAACTAACATGTAGTTACTAGTAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAACAAAATTTCTAACACTGAA

FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGGCCAGGAGCGACGTCA
 CCGCCATGGCAGGCATCAAGCTTTGATTAGTTTGTCCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT
 GGATGTGCCCTTCCAAATATACAAACAATACTGGCCCTCTTTGTTCTATTTTTTCAATCTTCCACCTATTCC
 ATACTGCATAGCAAGAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTTGAGGAACCTGGCACTCTTTC
 TTACAACGGCATTGTGCTGTACGCTTTTGGACTCCCTATTGTAATTTGCCAGAGCACACTGTGATTGATGGGGA
 GCTTGTGCACCTTTGTTCTCACAGGAACACAGTCATCTTTGCAACTATACTAGGCTTTTCTTGGTCTTTTGAAG
 CAATGACGACTTTCAGCTGGCAGCAGTGGTGAAGAAGAAATTAAGTAATTTGTCAAATGGACTTCTGTCACTT
 GTTGGCCATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGATTTTA
 GGTGCTCCCTTCTCACTTTTATTTGAAGCATACTATTTTACAGAGACTTGTCTGAAGGATTTAAAGGATTTTCT
 CTTTTGAAAAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTTGTGGTGTCTGCTGCAATTTAAATAT
 TTATGTGTTTTTCTGTTAGGTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCAATTGGTTAGGAATTCAGAATTCGCCCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATTTAT
 TAGCTCCATTATTACAAAAATTTATAAAATAAGTTTTTCACTGAGTCAAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTGCAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAACTGTTAATGCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTATTTTATGGAATGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAAATTTATGTTAACTTTA
 AGGTAAAGGTTGAAAAACATTTTGGAGATAAGGTTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGGAGAAGATGACATTGAAATCCAGTTTTTGAATCCTGTTTCTATTATAAGTGAAATTTGTGATCTCCTATC
 AACCTTTTCACTGTTTTACCTGTTAAATGGACATACATGGAACCACTACTGATGAGGACAGTTGTTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCTCTTTGACTTATTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAATATAGTTTAAATAACACTTAGAAGTGTTTACTTACCTGGAATAATTTGCTATGCCGTACATT
 CAGAGTGCCCTCCCTGCAAGGCCCTTGCCATGATTACAAGTAACTTGTAGTCTTACAGATGAAATTTAGCA
 TTAACAGTTTAAAGATTAGACCATGGTAATAGTAGTCTTATTCTTCAAGGTATATATCATATGTAATTTAAAG
 TATTTTTAAGACAAGTTTCTGTATACCTCTGAACCTGTTTGAATTTGAGTCTATCATGTATAGATCTGCTGTTT
 CCTTATAAAGGCATTTGTTGTGAGTTAATGCCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATTCACGTAACAGGCGATGATCAATTTATAGTGGTCTTTACATCTAATAATTTACAGGA
 CTTTTTTCAGGAGTGGGTATAAAAAACATTCAGTTGGTCTGACAGTATTTTGTAAAGATATTTGTTGTATG
 TTTATTCAGTATACCTACATAAAAAATTTATTCGCCATCAGCCAAAACCTAGTAATCATGACAGCTGTCTGTGT
 TTTATGAAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTCAAGCTTTTTTACTAAGATGCCATA
 AGCCACAGGTTTTATTGCTCAACTTAAGCCATGACTTTAGATATGAGATCAGCGGAAGCAGGAGCAAAATATCG
 CGGTGTGGCTGGAGCCTCCCACTGGAGGCTGAAGTGGCTTGTGGTATTATAAGTGTTCAGATTTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTGTGCTTGTGATCTACTGGACTGT
 TTTTTGCAAGAGTGCACTTCTGTGCTTCCCTATTTTCTGTTCTGGATGTCAGTGCACTGCTGCTACTG
 TTTTATCCACTTGGCCAGACCTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTCGATTTGGCAGCAAT
 GTGCTCTTGCACCTTGTATACAGCTTGACATAGTGTCTGCTGATTTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGATATGCACTGATACCAATACCATTCTCTATGGAAGAAAACCTTTTGATGATGAACAATAA
 AGATTTTAAATATCTATTTTAAAAAATAA

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FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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[illegible]

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDADFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSITSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

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FIGURE 197

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCAGGACCCCGTGCGCCGGCGCGCGCTTGAGTTCCCGGCGGACAAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTGCGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGGGGCCGCTACGCTTCACGGGCCGGGCGCGC**TGA**GCGTG
GGCCCCGAGGACTGCGCGGACCCGTGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVRRVSISALGRFTTRDEDLAVFLASR
AGRRLRFHGFGALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTC**ATG**GGACCAGTGAAACAGCTGAAGCGAATGTT
 TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT
 CTGCCTTTTGGTGGCATAACAAGGGACTTGCACCTTATCTTCTGCATTTTGCACTCTTTGGCA
 TTGACGTGGTACAGCCTTTCCTTCATAACCATTTGCAAGGGATGCTGTGAAGAAGTGTTCG
 CGTGTGTCTTGCA**TAA**TTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAG
 CTGGTGGACAGTTTTGTAACTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT
 TGCAGCAATGTGTTGCTTGTGATTCGAACATTTGAGGGTACTTTTGGAAGCAACAATACAT
 TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA
 TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATTCCCATGAATACAAAC
 CTATTAGCAACAGCAA
 AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCTCGCGGTTCCGGGGCGTTCCCTCCAGTCACCCTCCCGCGTTACCCGCGGCGCGG
 CCGAGGGAGTCTCTCCAGACCTCTCCCTCCCGTTGCTCCAACTAATACGGACTGACCGGATCGCTGCGAGGGT
 GGGAGAGAAATTAGGGGGAGAAAGGACAGAGAGCGAATACCATTCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAATAGTACTTCGAAATTTATCTTTGGTGCCTTCATACCTTGCTGCATGAGTCTTTC
 AACCCACTTTCTCTCCAACTAGACCAAGAAAGGTTCTACTAGTTCTTTTGGATGGATTCCGTTGGGATTA
 TATATAAAGTTCCCAACGCCCATTTTCATTATATTATGAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT
 TTTTATTACAAAACCTCCCTAACCATTAACATTATACCTTTGGTAACTGGCCTCTTGACAGAGAATCATGGGATTGTTGC
 AAATGATATGTTTATGATCCTATTTCGGAACAAATCTTCTCTGGATCAGATGAATATTTATGATTCGAAGTTT
 GCGAAGAGCGACACCAATATGGATCACAACCCAGAGGGCAGGACATACTAGTGGTGACGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTTCCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTGTGCCAAATTTGTTGAATGGTTTACGTCAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGCTGTCAATTCAGATATTGACAAAGAGTTA
 GGATATCTCATACAAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCACAAGTATCATGG
 AATGACCGCAGTGCTCTGAGGAAAGGTTAATAGAAGTTCAGCCAGTACCTGGATAAAGACCACTATACCTGATG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAATCAACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGTTGGCAGATTTTACAGAATAAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTACGCCATGGTCTGCTTCAGAAAGAAATTC
 TCAAAAGAGCCATGAATCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTTCTGGAATGTCCAGGATCTGCTCAATTGAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCTGGTAGTGTTAAACCAGCAGAAATGACCAAGAGGGGTATACCCCTTATTTCAATAGGGGTC
 TCTCTTGGCAGCATTTATAGTGATTGATTTTTTGTAAATTTCAATTAAGCATTTAATTCACAGTCAAAATCCATGC
 CTTACAAGATATGCATGCTGAATAGCTCAACCATTAATACAAGCTAATGTTACTTTGAAGTGGATTTGCATA
 TTGAAGTGGAGATTCCATAATTATGTGAGTGTAAAGGTTTCAATCTCGGAAACCAAGTTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGTGATACACACACACACACACATACACACACACAGGACCCAAA
 ATACTTACACCTGCAAGGAATAAAGATGTGAGAGTATGCTCCATTCTCACTAGCATAGGATAGATAAG
 ATCCCTGCTTTAATTTGGACTTGGCCAGATTAATGTATATATTAGCAACTTTGCACTATGTAAAGTACCTTATAT
 ATTGCACTTTAAATTTCTCTCTGATGGTACTTTAATTTGAAATGCCATTTTATGACAGTTATGCTTATAAC
 TTGATTGAAATGACAACTTTTTCACCCATCTCACAGAACTCTTATGCTGATTTTCACTGATAGGAGAAATTT
 TCTAATAATCCGAAATATGAACATAGAAATCTATCTCCATAAATTTGAGAGAGAGAAAGGTGATAGTGTGA
 AAATTAATATGTGATAACCTTTGAACCTTGAATTTTGCAGATGTATTCACAGCAGAAATGCAACTGTGGGCAT
 TTCTTGTCTTAATTTCTTCCAGAGAAGTGGTTTCTTATTTTCCCTCAAAGAGAGTCAAATCTGACAG
 ATTCTGTCTAAATATATTGTTTCTGTCTATAAAATTTGAGATTTCCGTGATGAGTCAATTTACGTGATTTTCA
 TAATTAATGAAGACACATGAATATCTTTCTTCTATATAGTTTCAAGAAATGGCCTGAATAGAAGCAACCGGCA
 CCATCTCAGCAATGTTTCTCTGTTTGTATTTGCTCCTTTGAAATTAATCACTTAATTAATCATTA
 AAATCAAATTTGGATAAAAAAAAAAAAAAAAAA

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FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVTPPHFYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIW
 ITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDKHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

GACATTTTGTGATCCGCATTTCGCTCCCACGGCGGGACCTTTGTAACTGCGGGAGGCCGAC
GACAGGCCACCCCTGCGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC
AAGGTGGCTCCCCTGAGAGGATGAGCAAGTTCTTAAGGCATTCACGGTCGTGGGAGACGA
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAAATGAAGAGAGAGGAGGAGGAGG
AGCAGCCACCACCACACCCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
CAGCTCCCACAGTCTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
TTGCTGAGCTCATCTTGACCTGAAGATCATCCAGCCGACAGAATAACTATGCTGCCATG
GTATTCCACTACATGAGCATCACCAATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAAT
ATTTGTCTTCCGCTGAGTTCTTTACCACAAGTTTGAGATCCTGGATGCCCGTGGTGGTG
TGGTCTCATTCCTGGACATTGTCTCTGTTCCAGGAGCACCAGTTTGGGCTCTGGGC
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTTCACTGCTCTGAGAAGCCCTGGACTTGATGAGTTTGTGTATC
AACCTGTAAGGAAGCTCTCTCCGGATGGCTATGGGAATGAAGAATCCGACTTCTACTCT
CACACAGCCACCGTGAAAGTCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
CAGGCTGGCATGTTCACTGGGCTGGTGTACACAGAGAACTGACAGTCACTGGCCAGTTA
TCACTTCAGATTACAAATCACACAGAGCATTCGCCTGTTTCAATCACAAGAGAACAAAAACC
AAAACTCTATAAGATATTCTGAAAATATGACAGAAATTTGACAAATAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

CGGCTCGAGCTCGAGCTGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAACAT
GCTCTGTCTGTGGCTGTAGCTCGGCGCGGTATCGGGGAAGCCAGACCGAGTTCAGTACTTTG
AGTCGAAGGGGCTCCCTCGCGAGCTGAAGTTCATTTTCAAGCTCAGTGTCTTCATCCCTCTCC
CAGGAAATCTTCCACTCCGCCAGCTGGAAGCAGAAAAATTTGACAAGCTGGAGATAAGGCCTT
TGATGGGCAGCTAGACTTTTGAAGAATTTGTCCATTATCTCAAGATCATGAGAAGAACTGA
GGCTGGTGTTTTAAAGATTTTGGACAAAAAGAAATGATGGACGATTTGACGCCAGGAGATCATG
CAGTCCCTGCGGGAGCTTGGGAGTCAGAGTATCTGAACGACGAGCAGAAAAAATTTCAAGACG
CATGGATAAAAAAGCGCACGATGACCATCGACTGGAACGAGGTGGAGAGCATACCACCTCCCTCC
ACCCCGTGGAAAAACATCCCCGAGATCATCTCTACTGGAAACATTCACAGTCTTTTGATGTG
GGTGAGAATCTAAAGCTTCCCGGATGAGTTCACAGTGGAGGAGAGGCACCGGGATGTGTGTG
GAGACATCTGGTGGCAGAGAGTTGGGGCGAGGGGCGGTATCCAGAAGCTTGACGCGCCCCCTGG
GACGCTCAGGTGTGCTCATCAGGTCCTAGTCCCTCCCGCAGCAACAACTGGGCATCTGTGGT
GGTCTCTCAGATGATTTCGAGAAGGAGGGGGCGAGTCACTTGGCGGGGCAATGGCATCAA
GGTCTCAAATTTGCCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC
TTGTTGGTATGACGAGGAGATCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCTTGGCA
GAGACAGCTCCAGACGAGCATCTACCCAAATGAGGTTCTTGAAGACCGGATGGCTGCTGGC
GAAGACAGCTCTACTACGGAATGCTGGAATCGGCCGACGAGGAGTCTGGCCAGAGAGGGGG
TGGCGGCTTCTCAAGGGCTATGTCCCCCAATCTGCTGGGATCATCTCCCTTATCCCGGCATC
GACCTTGACGTACGAGGAGCTCAAGAATGCTGGCTGCAGCACTATCGATGAACAGCGC
GGACCCGCGCTGTGTCTGCTGGCTGTGGCACTATCGCATACCTTGTGGCCAGCTGG
CCGACTACCCCTTGGCTGTGCTGGACCGGATCGAGGCGCAAGGCTCTATTGAGGGCGCT
CCGAGGTGACCATGAGCAGCTCTGTCAAACATATCTCGGGCAGGAGGGGCTTTCGGGCT
GTACAGGGGGCTGGCCGCACTTATGAAGGTCACTCCAGAGCTGTGAGCATCAGCTACGTGTG
TCTACGAGAACCTGAAGTACCTCGGCTGGGCTGCAATCGGGCTGAGCGGGGGAGGGCCGCCCG
GCAGTGGACTGCTGATTTGGGCGCAGGCTGGGGTGTGACGCATCTCATTTGTGAATTT
TGCCAACTCAAGCTGCTCGAGCGAAGCTGTGAAACCCCTAGACGCGACCCCGAGGGAGGG
GGGAGAGCTGACGAGTCCGAGGCTGTGCTGCTGACCCAGCAGACGCTCCTGTGTGTTTC
AGCGAAGACCAAGGAAATTTGAGAGGCTCAGAGGTGACGAGGCTCCGGGCTCACAATGGTGTG
GGACAGGACATTTTCTGCAGTCTGCTCAATGATGAGCTTGAGGCTGGAGGCGGCTGTGAT
TCTTCCATTTACCTTTCGACGCACTGCTGGCCAGCGGCTCGCTCTGGTCTGGCTGCTG
ATCTCCCTTGGCCCTTCTGCTGGCTGCTGCTGGCCAGCGGCTCGCTCTGGTCTGGCTGCTG
CCCACTCCCAACCCCTCTGCTCAATCCATTAATCAATGAGTGAAGTGGGAGAGGGCTACAG
CCAGGCGTGCATTTCCAACCTACAGCATGAGCCAAATGAGAGTGAAGTGAAGTGAAGTGAAG
GATCTGGCTTGTGCTGACTGTCATGAGCTTGTGAGCCCTGCTGATGCTGGTGGTCTGGGCT
TGGAGATCGAGGGGGCTGGGCTGCTGGCTGCTGGCTGCTGACAGAAGGCAGTGTGGGGCTT
ATGGTCTCTGAGCTGGCTGACCTTGTAGGATGGCCCACTCAGGACCAAGTCAAGTCTG
TCCCACTTGTGGCATGAGGCGATGGACACCATGTTTGAAGGCGAAGGCGACGCTGTCTG
GTGTTCTGGGGAGGGAAGAAAGTGTGGAGCCCTTAATATGACTTGTGGGAAGAGG
TTTTTGTCAAGAAGGACAAGCCGGAACAATGAGCGCACTTCTGTGCTTCCAGAGAAAGCGAGG
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTAGACCTGGGGTCTCTGCTCAAC
CCAGCAGGGGCGCAGCGGGACAGCCCAATCCATTTGTCTACGTCGTGGAACCTATTT
ATTTGTATTTTGAACAGAGTTATGTTCTTAATCTATTTTATAGATTTGTTTAACTTAATA
GCTGTGCTATTTCAAGTTTCATTTTATTCATATTTATGTTTCATGCTGATTGTACCTTCC
AAGCGCCGCCAGTGGATGAGGAGGAGGAAGAAGGGGGCTTGGCCGCTGCATGCATCAT
CTGCTTCAGAGAATTTCTTTGGGACTGAGGCAGAAAGCGGCCACAGGCACAGCCCTG
GCTCTTTTCCCTTTGGCAGGTTTGGGGAAGGGCTGCCCCAGCTTAGGATTTCAGGTTTGA
CTGGGGGCGTGAGAGGAGGAGGGAAGCACTAATAAGCTGAAGTGAATCGGATCGATTTCT
CTGCGCTGCGAGGATTTCTTTATTTCACTTTTCTGAATGTCAAGGACTGAGGTGCTCT
CACTGTGAATTTGTGTGGGCGGGGGCTGGAGAGGAGGTTGGGGGCTGCTCGCTCCCTCC
CAGCCTTCTGCTGCCCTTCTTAAACATGCGCGCAACTGCGCACTCAGGTTGCACTTCC
ATTTCCACCAGAATGACCTGATGAGAAATTTCTTAATAGGATCAAGAGATCAATGCAAAAAAT
TTTATATATGAACATATACTGGAGTCGTCAAAAAGCAAAATTAAGAAAGATGGACGTAG
AAGTTGTGCTTTTAAAGCAGCTCTTAAATAAAGTTGTTTCAAAGCTGAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIKFLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEI MQSLRDLGVKIKISEQQA EKILK
SMDKNGTMTIDWNEWRYHLLHPVENIPEIILYKWHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRNGNI
NVLKIAPESAIFKFMAYEQIKRLVGS DQETLRIHERLVAGSLAGIAQSSIIYPMEV LKTRMAL
RKTQYSGMLDCARRILAREGVA AFYKGYGVNPMGLGIIPIYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACMGTMSSCGGLASYPALVRTRMQQASIEGAPEVTMSSLFKHILRTEGA FG
LYRGLAPENFVKTIPAVSISYVVYENLKITFLRVQSR

Signal peptide:

amino acids 1-16

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTG
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTAGAGGCCGGACAGCAGTGT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTCCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCCTTGCCACAAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAAACAAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTGAAGTGTGTTAAGAGTGATAAG
 TAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCGTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTGTATATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCA
 CAAATTAAGCTGTAGTATGTACCTTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAAATGGGTCAAATGATTCACCTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVI VGNASRLKKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLSKASLCVSSFFAISWALLPLSPYMLK

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GAATTGTGTAAGACAGCGCGTGTGCCATGCGCGCTCTCTGGGGCAGGTGTTGGCTCTGGT
GCTGGTGGCCGCTCTGTGGGGTGGCAGCAGCGCGTGTCTGAAGCGGGCCTCCGCCGGCCTGC
AGCGGGTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCCCTCTTCTTG
AATACTGAGTACCTGATGCCCTTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC
CTTGGCATCGACAGATCTGACCTGGCTGTGCCATCTGTAACCTCTCTGGCTATCATCTTCA
CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAAAGTAAAGTTAGACTACTGC
GAGTGCGGGACGCAGCTCTGTGGATCTGCACATACCTGTGTTAGTTCCTTCCCAGAACCCAT
CTCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCTGCCCTTTCCTCTGCAGCTGTTTT
GCTTCCTTGTGGCCATCAGAGTTCCTTCCCTTGACAGCTCTGGAGAAAGACAGAGGCTGGG
GTTTGGGAATTGAAGACCAGACCCCATCTGAGCCCTTCTCCAGCCCTGTACCAGCTCCTACT
GGCATGGCTGAGCTCAGACCCCTCCTGATTTCTGCCTATTATCCCAGGAGCAGTTGCTGGCAT
GGTGCTACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGC
AACAGTCTACCCCTTGAGTGGGCGGAACCCACTTCCAGCTCTGCTGCCCTCAGGAAGCCCTT
GGGCCATGAAGTGTGGCAGTGAGCGGATGGACCTAGCACTTCCCCTCTCTGGCCTTAGCTT
CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAAGAGTGAAAG
AGTTTTGTAACCTTCAAGTGCTGTTCACTGCGGGGATTAGCAGCAGGAGACTCTACGCTCA
CCCTCAGCAACCTTTCTGCCCCAGAGCTCTCTTCTGCTAACATCTCAGGCTCCAGCCCA
GCCACCATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACT
CCAGCTGCATGGAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAACCGGAGGCCCTCTG
GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAAGGTGCGTCGGA
GTGGCAGCTGACAGGAATGAGCTGTCTATTAGCCTTGCTGCCCTCACCCTATGAGTGAGGCAC
AAATCCTCACTGCGACCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCGAGCCCACTGTAC
TCCAGCACCTGGCGAGTAGTGTCTGCTCAATAAATCTATGTAAACAGACAAAAAATAAAAA
AAAAA

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLLQEMKTLFLNTEYLMPFLLNQCSSLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVFPFPWTVVRKTEAGVWD

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FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTGAAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCTCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTCTGGGAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTT
 CAACGTCAGTAACGCCACCTGTGCAATTCTGTCTGGTGAAAAACAAGACTCTTGGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCACAGTCTGCACCAACCACT
 TCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAGGGTCTGGGGCTGCACTTTGCCCAGCACCCCAATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTTCCTGCTCTGCCCCGTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTTCATTATTA
 AAGCACTGGTTCATTCAGTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

00000000.11101

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSASSSSLETPVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGPWKCYEEECVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFECANVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRGLLP

0000270.11901

GGCCTCGGTTCAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCGAAGGTAGGAGGCA
GGGCTTGCCCTACTGGCCACCTCCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCCGCCG
GCGGCTGCTGTGGGTCTGCTGCTGAATCTGGTCCCCGGGCGGCGGGGGCCCAAGGCTG
ACCCAGACTCCGACCGAAATGCAGCGGGTCAAGTTTACGCTTTGGGGGCCCATGACCCGAG
CTACCGGAGCACCGCCCGAATGGTCTTCCCCGGAAGACAAGGATAATCCTTAGAGACGAGA
ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
ACGGTGTCCACCGGCTTTAGCCGGTCTGCCGCCATTAAACGAGGAGGATGGGTCTTCAGAAAG
GGGGGTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCCACTGCGACTCCCA
ATACAGCGGGGAGTTCCAGCACCGAGGTTTATGATCAATAGTCAGGAGCTGAAATCAGGCTG
ACTTCAAGCTGCGCGCTCCCCGGGAGGTCTACTGAGGACCTGACCGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACTGGGTCTACCCCGAGCCGGTGCCGCTCACCTCACCCACAG
CCATGCCATCTCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCT
TCGAGTTGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGCACCTATCAACAATGTC
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
GCCCTCTCAGAGCACCAACAGTACCAGGACCACTACTACCCCTTCCCCACCATCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCACTGTTTCACAGAGATGCAACCAATA
GACAGAAACCCAGAGGTAATGGCCACTTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
CTTGCCCTTTCAATCTTAGCCCCACTAGATATTTTTAGTACAGAAAAACAACTGAAAA
CACA

MVPAAGALLWVLLNLNNGPRAAGAQLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
 ILEDENDAMADADRLAGFAAEALLATVSTGFSSAINNEEDGSSEGGVVNAGKDSTREL
 PSATPNTAGSSSTRFIANSQPEIRLTSSLRSPRGRSTEDLPGSQATLSQWSTPGSTPSRWP
 SPSPSTAMPSPEDLRLVLMPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQRLTEHKPC
 TYQQCFPCRNLREECPLDSTLCTDNCASQSTSTRTTTTFFPTIHLRSSPLSPFPCFALA
 FWKVRIGLEDIWNLSLSVVFETMQAPIDRNG

CCGGGCTGCACCCACCGGCTCGGGGAGAAAGCATGCGCGGCTTGGCGGCGCGGTTGGTCTCTGCTAGCTGGGGAC
CGGCGCTGGCGAGCGGCTCCAGGAGCTCGGCTGAGCCGCTGACCGCGACTCGGCTATGCACTGCGAAGAGCA
GAACCTGCTCTGAGATGATGATGCTGATGTGGGTCAACCGTTGGGCTCTACCTCAGGAAGAGCTCAAAAGTGCC
CTCGGGACGACTGTGAATGATGATGCTGATGTGGGTCAACCGTTGGGCTCTACCTCAGGAAGAGCTCAAAAGTGCC
CAGTCCATGSGCAAGTGGCGCTCTTCCTCGGTTCTGTCTTTCAAGAGCGGCATCGGCCGTGGGCTGTTTCT
CATAGGCTCGGCAAGCTGGTGATGCTCTGCGCTACCCGACCTCTGTCGAGCGCTCTCTCCCATGTACCAAC
CTGTGTGGGCTTCTGCTGGGTGTCCTCATGCTGCTTGTGGTGCAAGCTCTCCACAAGGAGCACTGAC
CTCAGAGAATAAGTACACTTGTCTGTGCTCAGCTCTACTCTACATCAATCACTGCTGCTGCTGTAGGAC
CTGGGGGCTGCAGACACCGACTGTGGTACAGTCTCCGGGCTCTCTGCTGCTCATGCTGACGCTGCAGCTCT
CTTACTCGAGCTACCGCTCTGCATATGGTCAACAACTGTGTGGCCAACTGGGCTATGGGCTGSTCAACGTT
GTGGTGTGGCTGGGCTGGTGCCTGTGGAAACAGCGGGCGCTCAAGCTGCGCAAGTGGCTGGTGGTGTCTT
GTGCTGTGAGGGGCTCTGCTCTGCTCGAGTCTCTGACTCTCCACAGCTCTTCTTGGGCTCTGGATGCCATGCCA
TTGGACATACAGACACATCCCTGTGCACGCTCTCTTTTTCAGCTTTCTGGAAGTACAGACCTGTACTGCTGT
AAGGAATACAGAGGACAAGTTCAAGCTGCACTCGAAGAGCTTGGAGCGAGTCTGCCCCAGTGGGGATGCTGCCCC
CGCCTGCTGGCTCCTCTTCTCCCTCAACCTTTAGATATATCTCTCTTTTAACTTTTGAATTTGGACATGCA
AGGATGTGGGCGAGAATCATGTGCGAGCCGCCACCCCTCTGTGGCCCTCACCAGCTTGGAGTGTCTTTTAGG
AAGGCTCCAGCATCTGGGACTCGAGATGGGGAGGCCCTTACTCTCTGGAGCTGAACTGGGGTGGAACTGA
GTGTGTTCTTAGCTCTACCGGGAGGACGACTGCTGTCTTCTCCCAACAGGCTCTCCCAATCCCGACGTT
CTGGCTGGGCTCTGAAGCCCTCTGTCTACTCTGGGAGACAGGGAACACAGGCTTAGGGAATACAGGGGGTCC
CTTCTGTACCAACCCCAACCTCTCTCAGGACAACATAGTGTGTGCTGGATGTTGTCTTTGGCCAGCAGA
GGTTTACGCGGATCTCCCATGGGATCTTAGGGACCAAGCTCTGGGATGGGAAGGATTTCACTGCTGACC
GTGTGCCCTACGAGGTTCCAGAGAGGCTCACCATTCCCTTTCCAGGCGAGGCTCCAGCAGGCCAGGCA
AGGATCTGTGCTGCTGTGTGGTTGAGAGCTGCCACCGTGTGTGAGGAGTGTGGCCAGGCTGAGTGCATGA
TGACAGGCTGGCTGAGATGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGCGCATGTGTGAGACGGGTGTGT
CGGGGAAGAAGGTGTGCTTCAAGTGTGTGTGTGAGGGGTGGGTGTGTTAGCGTGGGTTAGGGGAAGCTGT
TGCGGCTGCTGTGGGGATGTGAGATGAGTGACTGTCGGGTGAATGTGTCCACAGTTGAGAGTGTGAGACGAGT
GAGGGAACCTGTGCACATAAATPACTTTGGAGCGAGGACTCTGCGCAAGCGCACTGGGCGGACAGC
CAGGAGCTCTCCATGGCCAGGTGCTGTGTGTGTCTGCTGGTGCCCTTTGGCCGCTCTCTCGCAAC
CTCAGAGGTTCCCAACAACAGTGGCTCTCAGAAAGCAAGCCCTCGGAGGACAGGAAGGAATAAGGATGGC
TGGGGCTCTCTCCATCTCTCTTTCTCTTGCCCTCTGCAATGGCTGGCTCTCCCTCCAAACCTCCATCTCCCT
CTGPGCCAGCCCTTTGCCATAGCCTGATTTTGGGAGAGGAGAGGGCGGATTTGAGGAGAGAGGGAAGAAGCT
TAGTGGCTGGGTCTGGTTCTTCTCCCTCCGACAGGGTCTTACTGTTCCAGGTTGGCCCGAGGCGAGGGGCG
ACATATGCTCGTGGCTGTGAAGGTGACCCCTGCATTTACAGACAGCCCTGGCATGTCTCTGCCACAGG
AATAGAATGGAGGAGTCTCAGAACTTTTCATCCCAAGGACGATCTCGGTGGTGTGAAGCAGACTGATTTTTC
CTCTGCCCTACCCCTTGTCCCTCTTTGAGGAGGGGAGCTATGCTAGACTCAACCTAGGACTCGGCTGGT
GCTCGGCTGAGTCTTTTGTATATAGAACTTTAAGGTGGAGGGTGCACAGGAGTGTCTTAATAAATCAA
TTCCAGAGCTCAAAAATAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPF SRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWVWLAWCLWNQR
RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCTGGA
 CTATGGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
 CTGATGGCCGCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC
 CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAGAAACCAAGCCGAGGAGGAGC
 TGGATGCCGAAGTCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
 CAGGCTGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGGAAGAGAGGCCAAA
 ACTCCAATATGAGGACAAGTTCGGAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCA
 ACACCTACACATCTCAGGATCTCAAGAGTGCCTGGCAAAATTCAAGGAGGGGGCAGAGATG
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCGCCCCATTGA
 GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGG
 TACGGCTGATCAACAAGTTCAATAGTTCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTC
 TTGATCTTGAATATATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGG
 TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCCCTGTAAGGAGTATGCTGCGT
 TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCAGGTGGAGGCCATCGAAGGGGGA
 GCCCTGCAGAAAGCTGCTGGTCATCCTGGCCACGGAGCAGCCGCTACTGCAAGAAGAAGGT
 CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCTATGCCAGCGGCACTTCTGAAGC
 TCGGGGGCTGCAGGTCTGAGGACCTGGTGACGAGAAGGGCACGGAGGTGCTCGCCGTG
 CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTCCGCCAGGAGGAGGCTGA
 GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
 GCCTGTGGGAACAGGGCTGGTGCGAGATCACGGCCACCTCCTGGCGCTGCCCGAGCATGAT
 GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGTACCG
 TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
 AGCTTGCTGAAGGAGCTGAGATGAGAGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
 GGCTGAGGGGTGCCAGCGTGGGTGGGCTTCTCAGCAGGAGGACATCTTGGCAGTGCTGGCT
 TGGCCATTAAATGGAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 218

MAPQSLPSSRMAPLGMMLGLLMAACFTFCLSHQNLKEFALTNP EKSSSTKETERKETKAE EEL
 DAEVLEVFHPHTEWQALPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSF GGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLR TLVQEKGT EVLAVRVV TLLYDLVTEKMF AEEEEAE LTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELGGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTCCCTCC
 CTTCCCGGGGCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTCGCGTTGCCACCCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCCTGTCCTGGTCAGGCCCCACCCCC
 TTCCCACTGACCAAGCCATGGGGGGCTGCGGTGTTTTTCGGCTGCACCTTCGTGCGGTTCCGC
 CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGACCCGCTTCGCGTTATCATCCTGGT
 CGCAGGGGCATTTTCTGGCTGGTCTCCCTGCTCCTGGGCTCTGTGGTCTGGTTCATCTTGG
 TCCATGTGACCGACCGGTGATGCCCGGCTCCAGTACGGCCCTCCTGATTTTTGGTGCTGCT
 GTCTCTGCTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT
 GATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCCTGACTTC
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTGGTGGTGGGAGTCACTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC
 TCTTGTGTAAGGACTGACTACCTGGACTGATCGCCTGACAGATCCCACTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTTCTGTCTCCTTCTCGTCT
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGAGCAGCCTGGGTTCAGCCAGTCACTGCTGGTGGGTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGCTGCTCTGCTCTCAC
 CCTGCCAAGACTCACCTCCCTTCCCTCTGCAAGGCCAGCGCAGGAGGACAGTCCGGTGAT
 GGTGTATTCTGCCCTGCGCATCCCAACCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTCTCCATCTCCAGTTCTGGACAGTGCAG
 GTTGCCAAAGAAAGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTC
 AGGCTGAGGGGGAACCATTTTTGGTGTGATAAAATACCCATAAAGTGCCTTTTTTCTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTTAAACCTCCTTGGGCTATATTTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTGGTCCCTTTCTCCTTGGTCCAGACCTT
 GGGGAAAGGAAGGAAGTGCATGTTTGGGAACCTGGCATTACTGGAACATAATGGTTTTAACCT
 CCTTAACCACCAAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAAGTGT
 ATCATTTTCTGCTGAGGGTGGAGTGCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGATTTTGTAAAAA
 AA

FIGURE 220

MGAAVFFGCTFVAFGPAPALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLEDGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIGHDSPYYFLTSAFLTAAILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLICKD

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AAGCTGTTTAAAGGAAGCAGAGGAGGGTTAGATTCTGTGAGTGAGGACGGAAGATCAACCCA
 TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTCGGNATCATCAGTGGTGTNT
 TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
 TCACCCATTANTTCTCGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTATAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

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FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTTCCCTTTCCCCG
 GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
 CCAGNTGGNGCGCCCTTCCCATTTGCCGTGCTCTGGTCAGGCCCCACCCCTTCCACNTG
 ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACCTTCGTGCGTTTCGGCCCCGGCCTTCG
 CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCTGGTCGCGAGGGGCA
 TTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
 CGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTCTC
 TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
 GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
 TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
 GGCCAGGTGTGGTTGGGATCCATGGAGACTACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCCTGTCTGGTCAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACCTTCGTCGCGTTCGGGCCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGA
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGTTGGCCCGT
 CCTGTGTTCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTTGGGGGTACAGAGCATGTT
 CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGTCAG
 GAAGAAAGTTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTGCTCCCACTAAAGATGTAGACCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGCTTGCTGGGTGGGGACAA
 CCAAGAGCCCCAAGTGCACTTCCCTAAGGTCCCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGGAGATTACCTTTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TGA**GTTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTTCAG
 ACCCTCATTCCTTCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCTGG
 GAACAATTTCCAAACTGTCCAGGGCGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAATAAAAAA

Abstract

FIGURE 226

Abstract

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCCGCGCA
 CAAGCCGCGAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGTGCTGGCCCTGGCTGTGC
 TGTCTGGCTGTAGCTGTCAACCGGTGCCGTGCTCTTCTGAACCAACGCCACAGCGCCCTGGTCACTGTGGA
 GCGGCCCCACCTGTCTGTACGACCTGGGGCTGCCAGCGCCCAACAGCGCCCTGGTCACTGTGGA
 AAGGCGGGACAGCTCGCACTTCAGCATCTCATTGACCGCGCTGCCCGGACCTCACCAGACA
 GCTTCGCAACGCTGGAGAGCGGCCAGGCTCGGTGCTGCAGGCGCTGACAGAGCAACAGGCCC
 CAGCCACGCTGGTGGGGACACAGGAGCAGGACCTGCTGGACACGCTGGCCGACAGCTGCCC
 CCGCTGCTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCCGAAGGGGACATG
 GCACGCTGGGCGAGGCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACTTGGTAACTCCGTGACGACATCTGGATGCCCT
 GCAGAGGACCGGGGCTGGGCCGCCCGCCGCAACAGGCCGAGCTTCAGAGAGCGCCTGCC
 GGGAAACCGGCCCGGGGCTGTGCCACTGGCTCCGGCCCCGAGACTGTCTGGACGTCTC
 CTAAGCGGACAGCAGGACATGGCGTCTACTCTGTCTTTCCCAACCCACTACCCGCGCGGCTT
 CCAGGTGTACTGTGACATGCGCACGGACGGCGCGGCTGGACGCTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAATCTCTCCGGGCTGGGACGCTACCGAGACGGCTTTGGCAGGCTCACC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACACACAGGCTGCCACAGCT
 GCACGTGGACCTGGAGGACTTTGAGAAATGGCACGGCTATGCCCGCTACGGGAGCTTCGGGG
 TGGCTTGTCTTCCTGGACCTTGAGGAGACGGGTACCCGCTCAGCGTGGCTGACTATTCC
 GGCAGTCAGGCGACTCCCTCTGAAGCACAGCGGCATGAGGTTACACCAACAGGACCGTGA
 CAGCGACCATTCAGAGAACACTGTGCGCCTTCTACC CGGTTGGTGGTACCGCAACT
 GCCACAGCTCCAACCTCAATGGGAGTACCTGGCGGTGCGCACGCTCTATGCCGAGCGG
 GTGGAGTGGTCTCTGGAGCCGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCGGCTCCGGGAGGACCG**TAG**ACTGGTGCACCTTGTCTTGGCCCTGCTGGTCCCTGTCCG
 CCCATCCCCGAGCCCACTCACTCTTTCGTGAATGTTCTCCACCCTCACTGTGCTGGCGGAC
 CCACCTCTCCAGTAGGGAGGGGCCGGCCATCCCTGACACGAAGCTCCCTGGGCCGTTGAAGT
 CACACATCGCTTCTCGCGCTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCCT
 TGCTGATGGGGCTGGCAAACTTGACGACCCCACTCTGCCCTGCCCGCACTGTGACTCCGG
 TGCTGTTTGGCGTCCCTGGCCAGGATGGTGGAGTCTGCCCGAGGACCCCTCTGCCCTGGCC
 GGCCAAATACCGGCATTATGGGACAGAGAGCAGGGGCGACAGACACCCCTGGAGTCCCTC
 CTAGCAGATCGTGGGGAATGTGAGGTCTCTCTGAGGTGAGGTCAGGCGAGTATCCCTCAG
 CCTCCCAACCGGGCAACCCCAACCCGTTTCCCTGGTGCCAGAGAACCACTCTCCCCAA
 GGGCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCTACCAGGCTCTGAGGTGAGGATGGG
 GAGCTGCTGCTTTTGGGAGCCACGCTCCAAGGCTGAGACAGTTCCTCTGAGGCGCCAC
 CCTGTGCCCGGCGAGGCTGGGGTCTGCAGTCTCTTCACTCTGTGGCCACCTGCTCTCTG
 TCTCAAATGGGCCCAACCATCCCCACCCAGCTCCGGCGCTCTCTTACTTGGGCGAGC
 CGGGGCTGCCATCCATTCTCTGCTCTGGAAGGTGGGTGGGGCTTCGACCTGTGGGCT
 GGACTGCGCTAATGGGAAGCTCTTGGTTTCTGGCTGGGGCTAGGCGAGGCTGGGATGAG
 GCTTGTACAAACCCACCAACCAATTTCCAGGAGCTCAGGGCTCTGAGGCTCCCAAGAGS
 GCCTTGGGGGTGATGACCTCTTCCCTGAGGTGCTGTCTCATGAGGAGGCAACCTTGGC
 ATTGACCGTGGCCACTTGACCCAGGCCAGGCCCGGCCGCGGAGTGGTCAAGGGACAGGA
 CCACCTCAGCGGCAAAATGGGCTCGGGGGACTGGGGACACAGGACCACTGGACA
 CTTTCTTGTGAATCTCCCAACACCCAGCACGCTGTCACTCCCACTCTTGTGTGCACACA
 TGCAGAGGTGAGACCCGAGGCTCCCAAGGACAGGCCAAGGGCAGGGCTGGAGCGGGG
 TCCTCAGCTGTCTGTCTCAGCAGCCCTGGACCCGCGTGCCTTACGTGAGGCGAGATGAGG
 CGGCTTTTCCAAAGGCTCTGATGGGGGCTCGAAAGGGTGGAGTCAAGCTTGGGAGCT
 GCCTAGCAGCTCTCTCTGGGAGGAGGGAGTGGCTTCTTCAAAGGACACCCGATGGCA
 GGTGCCTAGGGCTGTGGGTTTCCTTCTCCCTCCGCTGAGTCAAGTTTGTGCTTAA
 AACAAATAAATTGACTTGGCACCCTGGGGTGGTGGGAGAGGCCGTGTGACCTGGCTCTC
 TGTCACAGTGCCACAGGTCATCCACATGCGCAG

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FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDEQEELLDTLADQLPRLARASELQTECMGLRKHGHTLGQGLSALQSEQRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRRDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKXHSRMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCT
 TGCTTCCTGAAGTAGCTCACAGTAGCCCGGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAG**ATG**CAGGCCAAGTACAGCAGCAGGAGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAATCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGTCTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCACTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAATACTGTC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTCTGCAGCATGTGGC
 TGA AAAACTCTGCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTAACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAACTCTACCATGCTGAAGATAAACAACAAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGGCCCTTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC**TGA**TTTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTACACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCTATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTCTCTCAATGTCTAATATACCTCCCTGTTTTCTAT
 GTCTTCTTTACACTTGGTGGAATAAGAAACTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTTAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAG
 GTACTGAAGATTAAATAATAATAATGTAAATACTGTGAAAAA

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FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTNTGCAGCAT
GTGGCTGAAAACTCTGTCTGTGAGCTGTATAACAAAGCTGGAGGAAGTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

CCGAGCGCAGAAGAACTCTGCGCAGCCGACGACGACTGCTTGGAGGGGAATCGAGCGCGGGCTC
CGGGAACTTCGGCTTCGGGCCCTGCGCTTGTCTTTCGGGGAGGGAGCGGGCCCGCCCGCGGGG
CCCAGGCGCTCCGGATCCGCCCGCTCCCGGTCGCCGCCCTCGGAGACTCTCTTGGCTGCT
TCTGGGGTTTCGCCCGGGGCGGGGACCGCGGTCGCCGCCCTC**ATG**CGGGGATCTGCTGCTGCTG
TCGTGCTTGGCGCGCGCAGGGCCCGTGGCCGCTGGGACTTCTCCTGGGCTTCACTCTAGGCTCT
GCTCAGGCTCACTTGGTGTGAGGAGCCGCTCGGCCCGCAGGCCGCCCCCAACTGAGGACTCTG
AGCTGCGCGCGCGCGGCAACCAACCGCGCGCGCCGCCCAACTCGTGACGCCCGGAGCG
GAGCGCGAGAAGAGCCGGGCGCGGCAAGGCGCGGGGAGAATTGGGAGCCGCGCTTCTGCC
CTACCAACTCTGACAGCGCGGCGAGGCCCAAAGGCGCGTACAGGACCGGTACATCACTG
CGGAGCTTGGGCACTCAGGCACAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
ACGCTGGGCGTGGCCGTGAACCGCAGCTTGGGCGACCGGCTGGAGCGTGGTGTTCTCTGAC
GGGCGCACGGGGCGCGCGGGCCCCACTTGCATGGCAGTGGTGACGCTGGCGAGGAGCGGAC
CCATTGGACCACTGCACTTGGCTTGGCTTGGCCACTGCTGGAGAGCAGCGCGGACACTTTCGAT
TGGTTTCTTCTTGGTGCTTGAACCACTTACACGAGGACAGCGGCTTGGCACGCTTAATGG
CCACTCTAGCCTTGGCTTCGCCGCCCACTGTACTTGGGCGCGGCCCGAGCACTTATCGGCG
GAGAGCCACCCCGCGGCGCTACTGCTACCGAGGAGCTTTGGGTGCTGCTGTTCGCGATCTGCT
TGCTCAACAACTCGCCGCCCACTGGAAGGCTGCGCACAGCAATGCTCAGTTCGCGCGCTGGA
CGAGTGGCTGGGTGCTGCTTCTGATTCGATCGACCGGGTGGGCTGCACTGTGTACCAAGAG
GGGTGCACTATAGCCATCTGGAAGCTGAGCGCTGGGAGCGCAGTGCAGGAGGGGGACCTTCAT
TTCGAAGTGCCCTGACAGCCACCTGTGGCTGACCTGTGCACATGTACCAAGCTGCAAA
AGCTTTCGCCCGAGCTGAACATGGAACGCAAGTACACGAGAGATCAGGAGTATACGTGGGAGA
TCCAGAAATTACGACCATCTTGCGGCTTGTATGGGAGCAGCGGACGCTGCTTGGCCCGTGGGTAT
CCAGACCAATCCCGCGCGGCTCCGCTTTTGAAGTGTGCTGCGCTGGGACTATTCACGAGCA
GCACGCTTCTTCTCGCGCGGATGGCTCAACCGGCTGCCACTGCTGTGGGCTGACCGGGCTG
TGTGGCGGATGTTTGGGGAGACTCTAGAGGAGTGAACCGCGCTACACCGGCGCTTG
CGGCTCCAGAAGCAGCAGCTGGTGAATGCTACCGAGCTTGTATCGCGGCCGGGATGTGA
ATACAGCTGGACTTGCAGTGTGAGGACATGACCCCGAGGAGGCCCGCGGCCCTCACTC
GCCGAGTGCAGCTGCTCGGCGCGCTGAGCGCGCTGGAGATCTTGCTGTGCCCTATGTCACT
GAGGCTCACTGCTCACTGTGCTGTGCTTACTGTAGCTCGGCTGAGGCTGACTTGGCCCTTG
CTTCTTGAGGCTTTCGCACTGCAGCACTGAGCGCTGGTGATGCTCGGCGACCGCTGACCC
TGCTGCTATGTATGACGCGCCGAGGCCAGCGCTGGGCCATGCAGATGTCTTTCGCACT
GTCAAGGCCCCAGTGGCAGAGCTGGAGCGGCTTTCGCCGTGCCGGGTGGCATGGCTCAG
TGTGCAGACAGCTCCGCACTTCAACACTGCGCTCTATGGATCTACTCTCAAGAAGCAACCGG
TGACACACTGTTCTGCTGCGCGGCGAGACAGGCTGCTACGCTGACTTCTTGAACCCG
TCGCGCATGTATGCCATCTCCGGCTGGACAGGCTCTTTTCCATGCAATTTCAAGCCCTTCCA
CCGAGCTTGTGCCCCACCAACAGGCGCTGGGCCCCAGAGCTGGGCGCTGACACTGGCCGCT
TGTATCGCGAGGCGAGCCAGGAGGCGCTGCTTCAACTCGCACTACGTGGGACCGCGGTGGG
CGCTTGGCGGCGACTCTCAGAAACAAGAGGAGGACTGCTGGAGAGCTGGATGTGTACGAGT
GTTCTTCACTTCTCGAGTCTGCACTGTGCTGCGGCGGCTGGAGCGGCGCTGCTCGACGCT
ACGGGCGCAGAGCTGCAGCGCGAGGCTCAGTAGGACTGTATACCACCGTGCCTCCAGAGC
GTGCTTGAAGGCTCTCGGCTCCGAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGG
CAACAGCACT**TGA**CGCCCACTCTGCCCGTGGGCGCTGGCATGGCCACACCCCACTTCT
CTCCCCAAAAACAGAGCAACTGCGGAGGCTTGTGGGAGGCGTGGCGGTAGGCCAGACCC
AAGCTGGCCCACTGTTCCCTCTCTGGGCTTGTGGGTTCCTGGGCTTGGAACAAGCACTGGG
GGAGCTGCCCCAGAGGCAACCACTTCACTCCAAACCAAGTTTCCCTGCCCTTGAAGCTG
GCTGATTGGGCTGTGGGCTCCAGATTTATGATGAGTGTGCTGCTGACCGACCGACCGCTGC
CTTGTGGGCTTGGGGGCTGGGCTGTAGAAGATTGTTTGGGAGAGGAGGAGCTGAGGAGGG
GCATCTCCCAACTTCTCCCTTTTGACCTTCCGAGAGCTCCTTGCCTTTAATAAACTGGCCA
AGTTGGGAAAAA

MRASLLLSVLRPAGFVAVGISLFTLSLLSVTWEEPCGPGPPQPGDSELPGRGNTAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPHYPAQPGQAAKAVRTRYISTELGIRQRLVAVL
TSQTTLTPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
QHGDFFDWFFLVPDTTYTEAHGLARLTGHLASLAAHLYLGRPQDFITGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLLDATGVGCTGDHGBVHYSHLELSPGEF
VQEGDPHFPSALTAHPVRDPVHMYQLHKAFAAELERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDFYTEQHAFFSCADGSPRCPLRGADRADVADVLTGALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALT PQGGRRLPTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATALEPGDAAAALTLLLLYEPRAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTFLLAGPDVT
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPFELGRDTRGFRDQAASEACFYNS
DYVAARGRLAAEAGEEELLESLLDVYELFLHFSSHLVRAVEPALLQRYRAQTC SARLSEDL
YHRCLOSLEAGLSRTOLAMLLFEQFOGNT

GCTCTGGCCGGCCCCGGCGATTGGTCACGCCCGCTAGGGGACAGCCTGGCCTCCTCTGAT
TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTTAGAAAGCTTGATTTCTTTGAAGATGAAAG
ACTAGCGGAAGCTCTGCCTCTTTCCCAAGTGGGCAGGGAACTCGGGCGATTGGCTGGGAA
CTGTATCCACCCAAATGTCACCGATTCTTCTCTATGCAGGAAATGAGCAGACCCATCAATAA
GAAATTTCTCAGCCTGGCCGAAAATGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
AGGGTTGCTCAACGCCCCGCCTCATTTGAAAAACCAAATCAGATCTGGGACCTATATAGCGTG
GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCT
TTCCCCGCCCTGAGACCTCGACGACCATCTGTCAATGGCGGCTGGGCTGTTTGGTTTGAGC
GCTCGCCGTCTTTTGGCGGCAGCGCGCAGCGAGGGCTCCCGGCCGCCCGCGTCCGCTGGGA
ATCTAGCTTCTCCAGGACTGTGGTCGCCCGTCCGCTGTGGCGGGAAAGCGGCCCCAGAAC
CGACCACACCGTGGCAAGAGGACCCAGAACCAGGACGAAAACCTTGATGAGAAGAACCCA
GACTCCCATTGTTATGACAAGGACCCCGTTTTGGACGCTCGGAACATGCGACTTGTCTCTT
CTTTGGCGTCTTCATCATCTGCTGCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
GGATGAAGAGTGGTCCCGCGCGAGCTGAGAGCTGAGTGAATACCCAGAGGCCAATGGC
CTTCCCATCATGGAATCCAACCTGCTCGACCCAGCAACGATCCAGCTGCCAGAGGATGAGTG
ACCAGTTGCTAAGTGGGGCTCAAGAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
CTCTTCTCAGACACCTAATTAAAGGGGCTGAAAGTCTGAA

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FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPS AVAGKRPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

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FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCCTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACCTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCA
AGATCCAG

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FIGURE 237

GCGCGGGCT**ATG**CCGCTTGCTCTGCTCGTCTGTTGCTCTGGGCCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTGTCATCACCCGCTGCCTTCCGGGG
 ACGTAGCCGCGCACATTCCAGTTCGCGACGCGCTGGGATTCGGAGCTTCAGCGGGAAGGAGTG
 TCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCAATTCACACAAGGCTTTTGGAGGACCCGATACCTGGGGGCCACCCTTCTGCTG
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCGAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCGAAGGCAGGCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACAGCTACCACTCCCAAGGCAGTGCATATCCGCCCTGTTTGCAAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAAGTTGATTGATGCCTTC
 ATCAGGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTACCGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAACACAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCATCCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCCCAGTGCCCTTCTCTGC
 ATGCCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCACCCACCTCCTGGAGATGCTGATTAGCTGCCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACCTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCCTGGCCAAGCGGTGGCCAAACCTTATCGGCGCGCCCGAGGTGTCCCCCACTCT**G**AATT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAAGTCAAGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGCATTGGAATTTGAATTTAA
 CTTAGAAATTCATTTCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTGGTGGCTGCTGTATTGGACAGCAGAGAAAAGATTTCATCACCACAGAAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGCTCACTGTGTAGTGGA
 TGGAGTTTACTGTTTGTGGAATAAAACGGCTGTTTCCGTGGAATAAAAAAAAAA

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FIGURE 238

MPLALLVLLLLGPGGWCLAEFPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFVKPLGLANDTDHYFLRYAVLPREVVCTENLTFWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCARNARCTISISWELRQTL SVVFDAFITG
QGKKDWSLFRMFRTLTPECPLEASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPVPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIOFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLTPTDFSMYPYNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

CAAC**ATG**GGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCACAGTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCAAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACGTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGGAAAGAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCTTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAAGTGTCTCAGAA**TGA**TGCTGGGTCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTTGAGGGTCTGAGACTTGGAATATGGAAGAAGCAATACCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAG
TCCAGACCCAGGGACGGTACTTTCCTCTCTACCTGGTGCTCTCCTTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAAGTGCCCTTATAAGAGACCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACGTGTCAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCTGTGATCTTGGA**CT**TCCAGCCTCTAGA**ACT**GTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

0909279.111901

AAACTCAGCACTTGCCGGAGTGGCTCATTGTAAAGCAAAGGGTGTGCACCTCCTGGCCAGG
AAACCTGAGCGGTGAGACTCCAGCACTGGCTTACATCAAGGCCCCAGGACATGCAGAACTCTCC
TCTAGAACCGACGCCACCACTAGTAGTCTGCTGTGGAGATGCAGGCACCTGAGCCAAAG
CGTCCAGTGTCTTCTGCTTCTGGCTGTCTGGTCTCTTCTTCTCTCGCCTTGCCCTCTTTTA
TTAAGGACCTCTCAAAACAAGCTCTCCAGGCATCAACGCACAGAGAACAATTAAGAAAGGCTC
CTACAGTCCCTGGCAAAGCGCTAAGTCCACAGGCACCCACAAGGGCAGGAGGACAACCATCTA
TGCAGAGCCAGGCCAGAGAACAAATGCCCTCAACACACAACCCAGGCCAAGGCCCAACACCA
CCGGAGCAGAGGAAAGAGGCCAACAGGCACCCGCGGAGGAGCAGGACAAGGTGCCCA
ACAGCACAGAGGGCGAGCTAGGAAGAGCCAGAAAAAGAAAAACCATGGTGAAACACACTGTC
ACCCAGAGGGCAAGATGCAGGATGGCCTCTGGCAGGACAGGCGCAATCATGGAAGAGGCC
AGGACAACAAGACGACCCAGAAATTTGGGGCCAGACAGGAAGATGACGGCCTCTCAGGAGC
GTGTGACAGAAACACAGGGCAAAGCGGCACACAGGCAAGAGCTTATCCCAAAGATGCA
GCACGAATGCTGCGTCCCAAGAGGACAGTGTCAACAAGGCAGACAGAAAGGATGACCA
CAGCAGTCACTCCCACTTAAGGAGAAGAAACCTCAGGCCACCCACCCCTTGCCCTTTCCAG
AGCCCCACGACGAGAGAAACCAAGACTGAAGAGCGCCCACTTCAAACTTGAGCCTCGGTG
GGATTTTGAAGAAAAATCAGCTTGCAAAATAGGAGCCTCTCAGACAGTTCGCTGTACTCTG
TGAAGATCAAAAGCTCCAAAGTCTGCTGGCTCGAGAAAGCTCTTCTGCCCCAACCTCACTCTC
TTCTTGAGCTCCAGACACTTCAACAGAGTGAGTGGAGCCGCTGGAACACTTTCACACCTC
CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAGGTCGTGACACGCTTCCCTCCAG
TGCCCCAGCAGCAGCTGCTCTGGCCAGCCTCCCGCTTGGGAGCCTCCGGTGCATCACTGT
GCCGTGGTGGGCACTGGCGGCATCTGAAACAACCTCCACATGGGCAGGAGATAGACAGTCA
CGACTACGTGTTCCGATTGAGCGGAGCTCTCAATTAAGGCTACGAAACAGGATGTGGGGACTC
GGACATCTTCTACGGCTTTACCGCTTCTCCCTGACCACGTCACTCTTATATTGGGCAAT
CGGGGTTTCAAGAACGTGCCCTCTTGGGAAGGACGTCCGCTACTTGCACTCTGGGAAGGCAC
CTCGGCACTATGATGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAACCTTT
TCTGGTTCAGGCACAGACCCCAAGGAAGCTTTTCGGGAAGCCCTGCATCATGACAGGTAACCTG
TTGCTGCAACCCAGACTTCTTCGCATACATGAAGAACAGGTTCTTGAGGTTCAAGACCCCTGGA
TGGTGCCCACTGGAGGATATACGCCGCCACCCTCAGGCGGCTTCTGCTGTCTGCTGCCCTT
AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCTACTGAGGGCCATGAGCGCTTTTCTGAT
CACTACTATGATACATCATGGAAGCGGCTGATCTTTATACATAACCATGACTTCAAGCTGGA
GAGAGAAGTCTGAAGCGGCTACAGTACAGGAAGGATATCCGGCTGTACAGCGTCTCGTGGT
CCGGAAGCTCGAAAGCCAAGAACGACCCGCGGGCCAGGCTGCCATGGTCTCTTGCCTGCTC
CAAGGCACAGGATACAGTGGGAATCTTGAGACTTCTGGCCATTTCCCATGGCTGCAGACTAA
GCTCCAAGCCCTTCAGAGTTTCCAAGGGAACACTTGAACATGGACAAGACTCTCTCAAGAT
GGCAATTTGCTTAATGAGGTTGTGAGTTTCTTCAGTACTTCTGTAGGTTCTGAGGCCACCTG
GAATTTTAAATTAATGGGTTGATGGTGGCCAATACACAATTCGTGTGAAAAACACTGTT
CCAGTCCAAAAGCTTCTTGATACAGAAAAAGGCGCTGGATTACAGAAACATATAGATCTG
TTTGAATTTCCAGATCGAGTTTACAGTTGTGAATCTTGAAGTATTACTTAACCTCACTAC
AGATTGTCTAGAAGACCTTCTAGGAGTTATCTGATTTAGAAGGCTCTATACTTGTCTCTG
TCTTTAAGCTTTTGTCAACCTCTACGTGTTGTAGAAGAACTGATAATATACAAATGATTTGT
GTCCATGGAAAGGCAATAATTTTCTACAGTGAAGAAAAAAA

MRSLWRCRHL SQGVQWSLLAVLVFFLFALPSFIKEPQTKPSRHQRTE NIKERSLQSLAKP
KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDGRKEANQAPPEEQDKVPHTAQRAAM
KSPEKEKTMVNTLS PRGQDAGMASGRTEAQSWKSQDTKTTQGGNGQTRKLTASRTVSEKHQ
KAATTAKTLPKPSQHRMLAPTGA VSTRTRKQGVTTAVIPKKEKPKQATPP PAPFQSPPTQRN
QRLKAANFKSEPRWDFE EKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDLSRH
NQSEWDRLEHFAPPF GFMELNYSLVQKVVTFRPPVPQQQLLASLPAGSLRCITCAVVGNGG
ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGF TAFSLTQSLILGNRGFKNVP
LGKDVRYLFLFLEGT RDYEWLEALLMNTQVMSSKNLFLWRHRPQAEAFREALHMDRYLLLHPDFL
RYMKNRFLSKTLDGAHWRIYRPTTGALLNLALQCDQVSAYGFITEGHERFSDHYDTSW
KRLFIYNHDFKLEREVWKR LHDEGIIRLYORPGEPTAKAKN

amino acids 1-10

amino acids 11-35

amino acids 36-600

amino acids 481-496

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

CGATGCGCGGACCCGGGCACCCCTCTCTCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCAGAGTGGAATTTGTTCTCGAGATCTGAGGATGAAGGCAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTCAGAGAAACCTTCCATAGACTTTATCACACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGCAGCAGCCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCCTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCTCTATGG
ACAAGAGATTATTTTTCGACAGACTCTTCACATAGTCTTTGAGTTTGTGTATGTTGATG
CAGCTTTGCAGATATATATTGCATAAATCAGTGTACTTGCAGCTGTTATCTGTGCTACTTAAT

244/330

FIGURE 244

MRGPGHPLLGLLLVLGSPSEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

000000.1101
K0677.628860

FIGURE 245

GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCTTGCAGTCCCTTCTCTGGGAGG
 CCGGACCCCGCGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCGGGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGTGGGGGCTCCCTGGTGTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCGAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAAC TAGA
 ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAATAGTCCCTCTGCTCCCAAGATCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
 TCCGTGAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGGCGCAAGGGTAGGGCGGGCCCCAGAA
 CCCCAGGTAGGTAGAGCAAGAA**GATGGT**GTGTTCTGCCCCCTCAAATGGTCCCTTGCAACCATG
 TCATTTCTACTTTCCCTCACTGTTGGCTCTCTTAACGTGTGTCGAATTAATAACGACTTC
 CACTGAAACCATCTCCAAAACGTAGTGATGGGACACCATTTCTTTGGAAATAAAATACGACTTC
 CTGAGTAGCTCATCCGAGTTCAATTATGATCTCTTGATGTCATGCAAACTTACCACGCTGACC
 TTCTGGGGAACCAAGAGATAGAAATACAGCCGATGAGAGAGGGGAGCTGGAGAGAGGCTATCCGG
 TAGTCACCACTTCGCAATATCTAGGGCCACCCCTCAGGAAGGGAGCTGGAGAGAGGCTATCCGG
 AAGAACCCTCGAGGTCTCTGGAAACCCCCCTCAGGAGCAAAATGCACTGCTGGCTCCCGAG
 CCCCTCCTTGTGCGGCTCCCGTACACAGTTGTCACTATGCTGGCAATCTTTCCGGAGAC
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGTGAAGATACAGCAT
 CAACACAATTTGAACCCACTGCAGCTAGAATGGCTTTCCCTGCTTTTGATGAACCTGCCTTC
 AAAGCAAGTTTCTCAATCAAAATTAGAAAGAGAGCAAGGCATGAGGCATCTCCAAATATGCC
 ATTTGGTGAATCTGTGACTTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCTTCATCATTTCAGATTGTAGTCTGTGACGAAGATAAAC
 AAGAGTGGATCAAGGTTCTGTTTATGCTGTGCCAGACAAAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGGCGTGACTCTCTAGAAATTTATGGAGATTATTTGACGATACCGTATCCCC
 TACCCAAACAAGATCTTGCTGCTATTCCGCTTTTCAGTCTGGTGTATGGAAACTGGGGGA
 CTGACAACATATAGAGAATCTGCTCTGTTGTTGATGCGAAGAAAGTCTTCTGCTCAAGTAA
 GCTTGGCATCAAGTAGCTGTGGCCCATGAACCTGGCCACCACTGGTGTGGGAACCTGGTCA
 CTATGGAATGGTGAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTGTG
 TCTGTCACTGTGACCCATCTGAACTGAAAGTTGGAGATTATTTCTTTGGCAAAATGTTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCTGTGCTTACACCTGTGGAAATCCCTG
 CTCAGATCGGGGAGATGTTTGATGATGTTTCTTATGATAAGGAGGCTTTGATTTGGAATAG
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAGCA
 TAGTCTAAAAAATCAAAAAACGAGGACCTGTGGGATAGTATGGCACTATTGGCCCTACAG
 ATGGTGTAAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATTTCTCTCATCTCCAT
 TGGCATCGAAAGGGGTGGATGTGAAAACCATGTGAACACTTGGACACTGCAGAGGGGTGT
 TCCCTTAATAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCATACATGA
 AGGGCTCTGACGGCGCCCGGACACTGGGTACCTGTGGCATGAATGGCTATTACATTTGCATTAAG
 AGCAATCCAACATGGTCCATCGATTTTGCTAAAAACAAAAACAGATGTGCTCATCTCTCC
 AGAAGAGGTGAATGGATCAAAATTTAATGTGGGCATGAATGGCTATTACATTTGCATTAAG
 AGGATGATGGAATGGGACTCTTTGACTGGCTTTTAAAAGGAACACACACAGCATTCAGCAGT
 AATGATCGGGCAAGTCTCATTAACAATGCATTTACCTGTGAGCATTTGGGAAGCTGTCCAT
 TGAAGAGGCTTTGGATTTATCCCTGTACTTGAAACATGAAACTGAAATTTGCCCCTGTTC
 AAGGTTTGAATGAGCTGATTCCCTATGATATAAGTTAATGGAGAAAAGATATGAATGAATG
 GAACTCAATTCAGGCTTCCCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
 GACAGCAGAGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACACTACTCTCCGCTGTG
 TGCACAACATTCAGCGCTGCGCTACAGAGGGCAGAAGGCTATTTTCAGAAAGTGAAGGAATCC
 AATGGAACACTTGAGCTTGCTGTGCGAGTGACCTTGGCAGTGTTTGCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTTTCTTTGTCAGTACTGAGAAA
 GCCAAATTTGAATTTGCCCTCTGCAGAACCCAAAATAAGGAAAAGCTTCAATGGCTCATGAT
 GAAAGCTTTAAGGGAGATAAAAATAAACTCAGGAGTTTCCACAAATCTTACACTATTGG
 CAGGAACCCAGTAGGATACCACTGGCTGGCAATTTCTGAGGAAAACCTGGAACAACTTG
 TACAANAAGTTGAACTTGCTCATCTTCCATAGCCCATGGTAATGGGTACAACAAATCAA
 TTCTCCACAAGAACACGGCTGTGAAGAGGTAAAAGGATTTCTAGCTCTTTGAAAAGCAATGG
 TTCTCAGCTCCGTTGTGTCCAACAGACAATGAAACCATTTGAAGAAAACATCGGTGGATGG
 ATAAGAATTTGATAAAATCAGAGTGTGGCTGCAAAAGTGAAGAGCTTGAAGCTATG**TAAAAA**
 ACTAGTCCCTTGCCCGGTTCTGTTATCTCTAATCACCACATTTTGTGTAGTGTATTTTCAA
 TCTAGACATGGCTGTTTTGGCTCCAACCTGGAGATACTTTTTTCCCTTCAACTCATTTTTGA
 CTATCCCTGTGAAAAGAATAGCTGTAGTTTTCATGAATGGGCTTATTCATGAATGGGTA
 TCCTACCATCTGTGTTTTGTTTCTATCACAGGTGTGCCCCTGCAACGTAAACCAAGCTGTGGGT
 TCCTCGCCACAGAGAATAAGTACCTTATTCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE
 HPPQEIQIALLAPEPLLVLGYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPCEFDEPAFKASFSSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAAHELAAHQWFGNLVTMEWWNDL
 WLNFGFAKFMFVSVSVTHPELVKVDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDDG
 FCSRSQHSSSSSHWHQEGVDVKTMNTWTLQRGFPLITITVGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGHTTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKDRMNEVETQFKAFILRLRLIDKQTTWDEGVSSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC
 RTQNEKELQWLLDESKFGDKIKTQEFPPQILTLIGRNPVGYPALWQFLRKNWNKLVQKFELGS
 SSIAHVMVGTNTQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTITETIENIGWMDKNFDPKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGCAGGCGTGCTCTGCCAGTTTGGGACAGTTACAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATTGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGGCCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGACCACCATTATGACACACGGAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTC
 CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGGCCACTCATTTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACAAAAT
 GAGCATTACGGGCTGCGTGGCCCAACCTTCAGCTTCTTGTGTAACCACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTCACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGAGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCCACACAAATCATTCATATCTACTCACCTAACGCA
 AACTGGGGAGAGCCTGGAGCATCCGACTTGCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCTGTCCTTTCA

FIGURE 250

MSAVLLLLALLGFIPLPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLNHNTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC
PSC

0000270.11001

GCGACGGGCAGGACGCCCCGTTCCGCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTCGCGCT
CAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCTGTCACTGCTG
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCGTGCTGTGTGCAGATCCTCGTCCCTGG
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGAGCGGCTGGAGAAGTCT
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCTGTAT
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
TGGTCTTAATGGAGAACCAGGCGCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
AGATGGACAACAGGCTCTCTCAGCTGACCCAGCGAGCTCAAGTTTCAATCAAGATGCTGTCCG
GGTTGTGCGCAGGACGGAGAGCAAGATCTACTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
CGCCCGAGCTGTCTGCCAGGCGCGGGGGCGACGCTGAGCATGCCAAAGGACGAGGCTGCCA
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGCGCTGGCCCGTGTCTTCAATCGGCATCAAC
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
GAGAACATGTGAAGCCTCAGGCTGGGGCTGCCATTGGGGGCCCCACATGTCCCTGCAAGGTT
GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCTCTGTGAAGGGTGGAG
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAGATGGCCTATGCTTAAAGGAAAAATG
AAAGTGTTCTCGGGGCTGTCTCTGAAGAAGCAGAGATTTACCTACCTGTAGGTAGCCCCA
ATGTCTATTATGAATTATTACCCAGAATTGCTCTTCCATAAGCTTGTGCTTTGTCCAAG
TATACAATAAAATCTTTTAAGTAGTCAGTAGTTTAAGTCCAAAAAATAAAAAAAAAAAAAA

FIGURE 252

MRGNLALVGVLISLAFLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM

09989279.11904

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGACGAGGACACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGACGAAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAGACAGGACCTTTCTTACCCTTCAGTGAGGGTTCTCTGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCTTTTCTTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTTGGTGTGGAACATGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGAGCTGTAGAATACCCCTAGAGTTCTGTAGTGT
CCTCATATTAAAAATATAATGTCTCTCTATTCTTCAACAATAAAGGATTTTGCATATGAA
AA

FIGURE 254

MRIMLLFTAILAFSLAQSGAVCKPEQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFPSVRVPRPLHPNQLGSTGK
SSLGTEEORPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCGTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCCCTGGGTGGTGTCATCCCCCTTGGGGC
 TGCTGTTCTGCTGCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTACTCTCTTAGAGGAG
 CTGCTCAGCAAATACAGCACAACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGGTGTATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCT**TAG**ACTCCCGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGTCTTGCTACGT
 TGCCCAGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCGAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCTCTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACC GGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAAACTTCTCTCGTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAACCCACGTCCAGCCTGGGTAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAAA

FIGURE 256

MSCVLGGV IPLGLLFVFCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMSVAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GG SRLCSVLFVCFETGSHSATDAGVOWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGG
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTG
TGTCCTTCTTGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTCTGGTATGCTG

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FIGURE 258

MGSGPLVLVLLTLLGSSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHHVVCNT

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCGAGC**ATG**ATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCTTGCAGCTTTCTGCCCCCGCCGAGTGAC
 CCAGGACCCAGCCATGGTGCAATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAATGTACCAAGCAACAGGAGGCATACATTCAGAAGATTCGAAGAGTTCTCAAAAAATATA
 TCTGTTCATCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCCTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGGCTG
 ACGAGTGCATCGTATCAGAGGACAAAGCACTGGCAGAAATGTTGCTCCAAGAGCTGAAGAA
 GAGAAAAAGATCCGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGTACTTATTAATGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGAATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCACTTATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAAACCCAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAACACAGATCATTACAAACTCCAGACAAGAGAAA
 GCTGCCTCTGAAG**TAA**TGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTC
 TACAGGACAGTGAGGCTATAGCCCTTTCACAAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAATAACGTATGCCCTCTTTCACAAATGTCACTGGCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAGTTTCAACAAATGTCCATTACTCCCCCAA
 CCTCTGGCTCTCAAGATGACCACATTCGTATACAGCCTACTTCAAGCCTTTTGTGTTTACT
 GCTCCCCAGCATTTACTGTAACTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC
 CCCTAATATTCACCACTGGCTTTTCTCTCCCTTGGCTTTGCTGAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACTATTAATATTTCTTT
 CTTTTCTTTCTTTTTTTTGGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAATCC
 AGAGCTCAAGAGATCCTCCTGCCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCTTCCCTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAATATTAACATTGTAATATCGCTTT
 CCAGGTGTGGAGTGTTTGCACATCATTGAATTTCTCGTTTACCTTTTGTGAACATGCACAAG
 TCTTTACAGCTGTCACTCTAGAGTTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC
 TAGAAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTTTACGCCCTAAAAATAATAGTCTGTCCC
 TTTAGCCAGTTTTTCATGCTGTCACAAGACCTTCAATAGGCCCTTCAAATGATAATTCTCC
 AGAAACACAGTCTAAGGGTGAGGACCCCAACTCTAGCCCTCCTCTGTCTTGTCTGTCTCTGT
 TTCTCTCTTCTGCTTTAAATTCATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

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FIGURE 263

GGGCGCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTGCGAGCTCATGGGGCTGTCGGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG
 GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCCGGCCCGCTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTTCGGGATCCAGAAGCAGAAACAATATCAGCGGATTC
 GGAAGGAGAAGCCTCAACAACACAACCTTACCACCCGCTCCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCA
 TGAGAGCCAACTGGAGCTGGACCACGCCACCCTGGTGCCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCTAAAAAGCACAAAGCGCCTGTCA
 TCGACATTTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACCTGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGTCTACCATCAACACCAACAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTGTAGCCTCGTGTGGCTTCACCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGAGTTCCAGGAGGTGGTGCAGGCTTCGAA
 CTAAGAGGCCACTCCGCGGCTGTGCACTCGTTTGCTTTTCCACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGAAACTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTGCTGAAGACAGGCCGCTTTGAAGAGGCGGGGTGCCGCGCCGTGCCGC
 CTGGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCTATCTCTA
 CAATACCCGGCGGGGCGAGAAGGAGGAGTGTCTTGAAGCGGTCATGGCAGTGTATCGCCA
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCCTCTGTGGGACCGGGCGGTGCGGCTG
 TTTCAACACTCTCTGGCCACCGAGCCATGTTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCACAGGAGAGCACC CGCAGAGGCTGCAGCAGGAGTGACCCAGGCCCAAGAGACCTTGA
 AGAGCCTGGGTGCCCTGAAGAA**TGA**CTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCCTCATGGCACTGCTGCCATCTTTCTCCAGGTGGAAGCCTTTCAGAAGG
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTCTTCCATTGAACTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGTGCTGGCTGTGACTCCTCCCTGACTAGTGGCCAAAGTGCTTTTCTT
 CTCCAGGCCCAGTGGGTGGAATCTGTCCCACTTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAGAATGTGATTTTGGCCCTGTGGCAGCACATCTCACACCCAAAGAAG
 TTTGTAATGTTCAGAACACCTAGAGAACCTGAGTACTAAGCAGCAGTTTTCAGGAAGGA
 TGGGAGACTGGGATAGCTTCCCATCACAGAAGTGTGTCCATCAAAAAGACACTAAGGGATT
 TCCTCTGGGCTCAGTTCTATTGTAAAGTGGAGAATAATCCTCTCTGTGAACTCCTTGTGA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTTCCAATGCTGAAAGTGGTAAAGTGGGAACCGAGTGTGCTTTGAAACCAAA
 TTAGAACACATTCTTGGGAAGGCAAGTTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTTGGGAGATGATATCTGTTTAAAGGAGACCTTTTCAGTTTCATCAAG
 TTCATCAGATATTTGAGTGCCCACTCTGTGCCCAATAAATATGACTGGGGATTAAAAAAA
 AA

MELSQMSELMGLSVLLEGLLAMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQIRKEKPQQHNFTHRLLAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFPDCRAFIWVLANGDTLRVFKMTKREDDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKQVQLSTINTNQMNNTHAAVSPCGRFVASCG
FTPVDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWTDV
EYKKKQDPYLLKTRGFEEAAGAPCRLALSPNAQVLALASGSSIHLNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQHLKRASNESTRQRLQQQLTQ
AOETLKSLSGALKK

Signal peptide:

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTCACCCCAAGTGACC**ATG**AGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACTGTGTGCTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA
 AGCACACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGTGTCTCCATGGACTTGAAGAACATCAATTTT**TAG**CGCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCTCCCTCCCTCCCCAGGTGACCTGCTCTCTTTCTGGGCCCTG
 CCCCTCTCCCCACATGATCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCAGGTCCTGGCCTGACCTCAGGCCCTCAGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCACAGCTTTTCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
 CAACTACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

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FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACCTTGAGAAATGTCTTTC
 CTCACAGGACCCAAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACCTTTCAAA
 GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTCTGTGGTGGGATCA
 GGAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTCATGGGATGTATT
 GTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTGTTAGGCCCTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTGCGAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCCTGCCAACCCGCCACCCAGCCC**ATG**GCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCAT**CTAG**GTCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 271

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT
 TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTCTGTCTACTATTATTATTGTTG
 GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
 ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
 CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
 GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
 ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
 TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
 TTATTAATTTTAAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
 TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
 ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
 AGAAGGGAAAATGTTGCCAAGGAAAAA

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FIGURE 272

MTFFLSLLLLLVCEAIWRNSGSGNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 275

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAGACCATTACGTCCTCCCGG
 GGCAGGGGTGACAAACAGGTGTCTATCTTTTGTATCTCGTGTGGGTGCTCTTCTTATTTCAAAGGAAAG
 ACCCAAGGTAAATTTTGTACCCAGGAGGACATGATGTAGCCACCTCTTAACCTTCCCTTTCTTGAACC
 CCCAGTTATGTCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTT
 GTGGTTGGAGGAGAACCTTTTGGGGCTGCGTTCTCTTAGCAGTGTCTCAGAAGTGCTCAGAAGTGACTTGCCTGA
 GGGTGGGACGAGAAGAAAGGAAAGGTCCCTCTTGTCTGTGGTGCACATCAGGAAGGCTGTATGGG
 AATGAAGGTGAAAACCTTGGAGATTCACTTCAGTCAATTGCTTCTGCCAGAGATCATCTTTAAAA
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAAGGAAATGGATG
 CAAGCAGCTCCGGGGGCCAAACGCATGCTTCTGTGGTCTAGCCCCAGGGAAGCCCTTCGGTGGGG
 CGCCCGGCTTGGAGGATGCCACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGGTTCGCC
 GGGGGCTGCTTGGCTGGATTTCGCCGGTGGTGGTTTTCCTGGTGGTCTCTCTGCTGTGCTATCTCTGT
 CCGTGTAGATGTTGGCTGTGACCCCAAAGGTGACGAGGAGCAGCTGGCATGCCACGGGCCCACAGC
 CCCAGGGGAGAGGGGTACAGGCGCTCCTTCAGGAGTGGGAGGAGCAGCAGCCCAACTCTAGTGA
 GCAGCCTGAAGCGGCCAGATCCACAGCTCAGGAGGAGCTGACAGGAGCCCCAGAGAGAAACCCAG
 TGGGCATACCAAGCCAGCATGCTCTGCTGGCTGGGTCTGACAGGAGCCAGAGTGAATGCTGGCTCAGCTGG
 CGCGACCTCTGGCTTCCGCTACTCCAGGTGGACAGGCGAGAGTGAATGCTGGCTCAGCTGG
 CCACAGAGTATGACGAGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACAGCTGGAGACGTG
 CCTTACCCGCCACCCCGAGGAGAAAGCTGTGAGGAAGGACAAAGGGATGAGTTGGTGGAAAGCCATT
 GAATCAGCCTTGGAGACCCCTGAACAATCTTGCAGAGAAACAGCCCAATCAGCGTCTCTTACACGGCTCT
 CTGATTTTCATAGAAGGATCTACCGAAGACAAAGGACAAAGGGACATTGTTAGCTCACTTTCAA
 AGGGGACCAACACAGCAATTCACACGGCTCATCTTATTTCGACCATCAGCCCATCATGAAAGTGA
 AAAATGAAAAGCTCAATGCCCAACACGCTTATCAATGTTATCGTGCTCTACGACAAAGAGGGTGG
 ACAAGTCTCCGGCAGTTCATGCAAGTTTCAGGGAGATGTGCATGTAGCAGGATGGGAGAGCTCCATCT
 CACTGTGTTTTCCTTTGGGAAAGAAAGAAATAATGAAGTCAAAGGAATCTTGAAGAACCTTCCAAA
 CCGTCCAACTTACAGCACTTTCAGCACTTTCATCCAGCTGAATGGAGAATTTCTCGGGGAAAGGGACCTTG
 ATGTTGGAGGCCCTTCTGGAAGGAGCAGCTCTCTCTCTTTCTGTGATGTGGACATCACTTT
 CACATCTGAATTCCTCAATACGTGTAGGCTGAATACAGCAGGGAAGGATTTTATCCAGTT
 CTCTTTCAGTCAGTCAATCTCTGGCATAATATACGCCACCATGATTCAGTCCCTCTTGAACAGC
 AGCTGGTCATAAAGAGGAACCTGGATTTTGGAGAGACTTTGATTTGGGATACGCTGTCTCATTCG
 GTCAGACTTCATCAATATATAGTGGGTTGATCTGGACATCAAAGGCTGGGGCGAGAGGATGTGCAC
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGAGCCTGTGGAGGACTCTTCCACC
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGTACAAGATGTGCATGCAGTCCAA
 GGCCATGAACGGGCATCCACGCGCCAGCTGGGCATGCTGGTGTTCAGGCACAGAGATAGAGGCTCAC
 CTTCTCGAAACGAAAGACAGAGCAAGTAGCAAAAAAATCAAGTACCCAGAGAAGGATTTGGGGAGA
 CACTTTTTCTTCTCTTTGCAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATATAAGGAGC
 ACRAAGAAATTTGAGTGTGGGTGAGAGATGAGAAAGCCCTCCGATTTCTCTCTTGTGGGCTTTTTAC
 AACAGAAATCAAAATCTCCGCTTGGCTGCAAAAGTAAACCCAGTTGCACCTGTGAAGTGTCTGACA
 AAGCCAAATGCTGTGAGCTATAGCCTTAATGGTGGAGGTTTGTATGGTGTGTTTACAATACAT
 GAGACCTGTGTTTGTGTGCTCATTTGAATTCATGATTAAGAGAGTTTCTGARAATAATTCAT
 TAGCATGAAAGCAAGCATATTTCTCCTCATATGAATGAGCCTATCAGCAGCGGCTAGTTTATAGG
 AATGCTAAAAATCAGAAGGCGAGGAGAGGAGATAGGCTTATTATGATATACTAGTAGATCAATTAAGTA
 AATAAATATGGACAGAAAGAAAGAAACCAATAAATATCGTGTACATTTTCCCAAGATTACCA
 AAAATAATCTGCTTATCTTTTGGTGTGCTTTTAACTGTCTCCGTTTCTTTCTTTTAAAAAT
 GCATTTTTTTTTCCCTTGTGAGTTATAGCTGCTTATTTAATTACCATCTGTGTAACAGGAGA
 GCACAAGTTGGGCTCATTTTTATTTTTTAAAGAGATCACTTGGAGTGATTTAGGAACCTTGA
 GTTCAAGCATCAATTTGATGCCATATCCAAGGACATGCCAAATGCTGATTCCTGTGAGGCACTCAAT
 GTGAGCATTTGAGACATAGGGAAGGAATGGTTGTACTAATACAGACGTACAGATATCTTCTGTGA
 GACTATTTGAGAGGAGCAACTGAACCTGGAGGAAAGAAATGACACTTCTGCTGTACAGAA
 AAGGAACTCATTCAGACTGTCTATCTGTATGTACCTAAAGTCAGAAACACCATTTCTCTCTCA
 GAAGTAGGAGCCGCTTCTTACCTCTTAAATTAACACCACTATACCTGTGTAACCAACATATATAT
 TTTCAAAACAGGCTGCTCCTCTCGGCTTCTGCTTCCATTAAGAGAAATGAGGAAATATATATAT
 ATATATATATTTGGAAGATCAATCCATCTGCCAGAAATCTAGTGGGATGGAATTTTCTGCTAT
 GTTATCCACCACCGGCGAGGTGAAGTAACTGAATTTTAAATTAAGCACTTCTACTCAATCA
 CCAAGATGCTCTGAAAAATGCAATTTTATTACCATTTCAAACATTTTAAAAAATAAATACAGTTA
 ACATAGAGTGGTTTCTTTCATCTGTAAGAAATTTATGACAGCAGGATGATGAGTCAATATCT
 TTTTGGAGTCTGCTTCTGTTTGTCTCAGATAAATCTGATTTTAAAGCTTCAAGAACATTCAGC
 GTTGTGGTGTGTTAAAAAATGCAATGTATGATTTGATCTGGTATGTTTGAATTTAATTAACAC
 AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAATGCTTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACC GGATCAACAATGCCTTCTTTCTAAATGACCAAAC
 CTGGAATTTTTAAAAATCCCTTCCACACTTGACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTGCTTCTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTCCTCTTTTGTAAATAAATTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACAGAC
 TCAAAATATTCTAAAAATTTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTTGTTGACCATTCTTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTAAAAA

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GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTACCACCA**ATGA**AGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGTACTGGTCTGTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGCTCC**T**
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACTATTATGCTTCCTGTGATTTC
ATCCAAC**T**ACTTACCTTGCTACGATATCCCTTTATCTCTAATCAGTTATTTTCTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTCTGGGTGAGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
 GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACACAGGCTGG
 ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCCCAAGAGCTTTCATTGTATCTATTGATTTTACCACATTAGCAATTAACCTGAGAAAT
 GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCTTGTCTACTAAAAA
 TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGAGGCTGAG
 GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTCGGGTGAGCCGAGATCGCGCCGCTGAT
 TCCAGCCTGGGCACAAGAGTGAGACTCCATCTCACACA

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVVERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

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GTCA**ATG**CCAGTAGCCTGCTCTGTGCGCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCCTGCTCTTCCATGG
GACCCTGCACTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGAGC
CGGGGCCGGGATGCAGCCAGGAACCTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGGCC**TGA**ATCTGCCTGGATGGA**ACT**GAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCGGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
CAGGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTCACTGCCTACACACCCCTATTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLFFHGTLLQGQALNGVYRTTEGRLTK
ARNSLGLYGRTEILLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQHRRLQ
IQERLHTAALPA

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FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAAATTTGCGAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATGAAAAGCTC
 TGGACAGAAAGTCAATGCCCTTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAATGTGTCTTCTCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCTGTGCGAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAA**ATAG**TGCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAATAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTTCTCTAGTCTTTCTCACTTGACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGAATAACAAAAATTCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC
 TTGTCAGCCCATTACCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTCTGATTTGATTTTTTTTTTTCTTCTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTTCCACCATTGCATTACAACCTCTAACTTAAATGGGTAACCCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAAATGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTT
 TGGAGCTGAAAACCTGAATTAAAGAATGCTATCTGGAAAATGCATACGCTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAGCAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACTTTAACTACACATGCTTGGAAATTAAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRS LPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRS SKRYICEFTIPK

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FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCTCCGCGCGC
 CCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
 GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
 GAGTCGGCGGCGAGGCCGGGGCCGGGACCC**TGG**CCAACCCCTCGGCACCCCTCAACCCGCT
 GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCAGAAAGT
 GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
 GCCCTGACAGTGTTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
 CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCTT
 CTCATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAFLVGSAPVAPVAALESAAEAGACTLANPLGTLNPLKLLLS
SLGIPVNHLIEGSQKCVNELGPQAVGAVKALKALLGALT VFG

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TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC
TCTTGGCCCTCCGACAGCGCATCAAGTGAAGGTGGTGCCAGTCTCTCGCTCCGCTCCGCT
GCACAGGTGGCTGGTACCCGGCTTGGCCCCAGTCTCAGTGCACAGAGACCCAGCCCC
TCAGACACAGACACAGCAGGGTATGTCAGGCTCCGAGGGAGGAAGAGGAAGATGAGCAGGAGG
CAGACGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGTCTGATGGCCAGCAGGACGAGCTT
GCCAAGGACACTTCAAACCTCGGATTCAGCTGCTGCCAAAGATCTCCATGAGGCCACATGG
CAACATGGTCTTCTCCTCAATTGGCAGTGTCTTGCCATGCAGGCTTGATGCTGGGGGCCA
CAGGGCCGACTGAACCCCAGATCAAGAGAGGGCTCCATTCGACGCCCTGAAGCCCAACAG
CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCCTCTCCCGCAACCTGGAAT
GGGCCCTCCACAGGGGAGTTTGGCTCTATCCACAGAGTAATTTGATGCTCAAGAGACTTTCT
TCAATTTATPCAAGAGGATATTTGATACAGAGTGGTGCGCTATGAAATTTGCAATGCCCTCA
CAGGCCAAAGGCTCATGAATCAATCATTAACAAAGAGAGCTCGGGGGGAAATTCCCAAT
TTTGTAGATTAATCTGAACCAATTAATCTTGATGATACATCTGTTTCAAAGGGA
AATGGTTGACCCCATTTGACCTGTCTTACCGAAGTCGACACTTCCACCTGGACAAGTAC
AAGACCAATTAAGTGGCCATGATGTACGCTGACGAGCAAGTTGCTCCACCTTTGACAGCA
TTTTCGTTGTGATGTCTCAAACCTGCCCTACCAAGAAATGCCACCATGCTGGTGCTCTCA
TGGAGAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
TGGCTCAGAAACATGAAACCAGAAACATGGAAGTTTCTTTCCGAAGTCAAGTGATGATCA
GAAGTATGAGATGCATGAGCTGCTTAGGACAGATGGGAATCAGAAGATCTCTCACCTTTG
CTGACCTTAGTGAACTCTCAGCTATCGGAAGAATACTCCAAGTATCCAGGTTTATACGAGA
ACAGTGATTGAAGTGTATGAAGAAGGGCAGTGAGCGAGTGGCAGGAATCTGTTGCAAAATTAC
TGCTTATTCCATGCTCTCTGTATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
AAACCTCTGGAATGCTTCTGTTTCTGGGACGGGTGGTGAATCGAGCTCTCCTATTAAGTACG
ACATGCATAGACCATCTCGTGTGTAGTAGATCTGAAATCTGAGGATACAAACACACAGGA
TACAGCAATGATGGCAGGGAGAGGTGTCCTTTGTTCTTAACATAGTTTAGGGTGTTCT
AAATTAATATCAGTAGTCCCCCTTATCTGAGGGGATACATTAAGAAGCCCCAGCAGATGC
CTGAAACGGTGACAGTGCTGAACCTTATATATATTTTCTACACATACATACCTATGAT
AAAGTTAAATTTATAAATTAGGCACAGTAAGAGATTAACATAATAACACATTAAGTAAAA
TGAGTTACTTGAACGCAAGCATGCAATACCATTAACGTCAAACTGATTATAGAGAAGGCTA
CTAAGTGACTCATTTGGCGAGGAGCATAGACAGTGTGGAGACATTTGGCAAGGGGAGAATTCA
CATCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCACTACTCAGAATGGCATGC
TGCTTAAGACTTTTAGATTGTTATTTCTGGAATTTTCATTTAATGTTTTTGGACATGGT
TGACCATGTTTAATCGAGACTGCAGAAGCAAAACCATGTTAATGAGGAGGACTACTACAAA
GCATTAATTTGATACATATTTTAAAAAAGGAAAAAAGAAAAA

FIGURE 292

MKVVPSLLLSVLLAQVWLVPLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGE
EEKAWLMASRQQLAKETSNGFSLLRKISMRHDGNMVFSFPGMSLAMTGLMLGATGPTETQI
KRGLHLQALKPTKPGLLP SLFKGLRETLSRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
DTECVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLIIVDYILFKGKWLT PFD
VFTEVDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL
ALEDYLT TDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRIRIFSPFADLSELSA
TGRNLQVSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDPRPFHFMIEETSGMLLF
LGRVVNPTLL

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FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGAC**ATG**AG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCAG**TAG**GGCTCCAGGGGCCATCACTGCCCCGCCCCTGTCCCAAGGCCAGG
CTGTGTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 294

MRRLLLVTSLVVLLWEAGAVPAKVPVKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPPEEDQDHIYHPQ

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AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGC
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACA**ATG**AACCAACTCAGCTTCTCTGC
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCCTCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATTATCACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCTTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCACTGCGGGATT
TGTTCAAGTTCAGGGTATTTAATAACGAGAGAGAGGCCAACGCCTTGTTGTCTGGAATGAGGG
TCACCGGATGTAAACACTGAGCATCTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
CCCGACAGTGTGGAGATTTTCTCGTGTTTGATTGGAGTGATATGGAACATCATGTTGGTTA
CAGCAGCAGCGGTGAGATAA**CT**AGGACAGCTGTGGCTTCTATCATCGT**TCG**AGACGTTTTGTG
GGAGGGAACCCAGACCTCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTACCCA
GTAGCTAGAATGTTAATGGCAGAAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYS PYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEAS PQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGAACTCGGCGCGGAGGTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGCCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAATATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATCTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTGGCT
 GGGGTGGGGCATTGGTCACATATGACCAAGTAATTGAAAGACGTCACTCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

MGLGARGAWAALLLGLQLVALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTMTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVQN
TSQISTSTMVTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSEVGGIVLTGLVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGGACCCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTCCGTGCTGCTGCTGGC
 GCAGCTGTGAGACGCCGCCAAGAATTTGAGGATGTGAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATCTGGGCATATTTATAATAAGAACATATCTCAGAAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAAATATGAAGAAAGAAGCTCTGTACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTTGGGGATCACCAGCCTTT
 TGCAAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGCTTTTGACCGG
 CATGTTGTCTCAGCTAAATTGGGAATTGAATTCAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTGTGATTTCACCAACT
 GTTGCTGGAAGATTCAAAACCTGGAAGCAAAAACCTTGTCTGATTTTTTTTCTGTGTAACGTA
 ATAATAGAGACATTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTG
 TGACTTTTACTAATAAAAAATAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTTGTTTGTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
 AACAACTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
 ACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACCTCATGGTAAACGGGAT
 CTAAATGCCTGGTGGCTTTTACAAAAAGCAGATTTTCTTCACTGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTGTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACT
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT
 TCTTCCTATGTCTCTTTTGAATGTAACAAATAAAATAATTTTTGAAACATCAA

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FIGURE 300

MATLWGGLRLGSLLSCLALSLLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHYINKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTTTTIYLSIL
GLLLLYMVYLT
LVEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLA
RSRANVLNKVEYAQRWKLQVQEQ
RKSVFDRHVVL

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FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTCGCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCATGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTA AAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTAA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAAGTGTTTTGCCCCAAAATTCACTAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILI
ILHQ

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FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGC**ATGT**TTTTGCCCACTGAAACTCATCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTACGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
AGACTGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTTCA
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC GCGTACACTTGATGGGGACATCTTATGC
AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG
AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAGAAAACCATTTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTTGTGGGAATTGTC
TGTGCCACAATCCTGCTGCTCCCTGTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
GAGTTCAGTGAATTTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGG
GAATGCCAAAAACACAGCAAGCCTTT**TGAGA**GAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCCTGTGTGTGCTTGGGCCACTCTACCAGTGATTTAGACTCCCGCTCTC
CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCTCAAACCCCCGTT
GGATCAGACCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLG LNDLNVSPPELTVHVGD SALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQGT YICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLRMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPVLILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEKPC HFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNNLEKKSGGGMPKTQQAF

000000-11101

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
 GTTCTACCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACACATTTTGC AAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATGCA**
 GGATGAAGATGGATACATCACCTTAAATATTTAACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTGCGGCTGGTGGCTCTGGGGATTTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAACAATCAGAATAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCGTGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGCTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA
 TGGAAAAGGAAATATGAATGTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
 AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATGTGACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

306/330

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWVRVMAILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLLRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

09089279.111901

CCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGCATCCCGC
CCCGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGGGAGCCGACCGC
CGCCGAGGAGCTCGGACGGCATGCTGAGCCCCCTCTTTGCTGAAGCCGAGTGCGGAGAA
GCCCCGGGCAACGCAGGCTAAGGAGACCAAGACGGCGAAGTCGCGAGACAGCGGACAAGCA
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGACGCAAAAGAACGGTGGTGGTGGG
CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGACGAGCCCCAGCAAGAGCAAGACCAGTGC
GACAAAAACAGTTAAATGCTTTTCCGGGTCAAACCTCTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACGACAGGCTCAGTTATAGGTAATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCACTGCAAGCCGATGGAACCATTTGATGCGACCAAGATGAGGACGACATCTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAATATATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGCTCTTGGCGTGTGAACGGAGGCAAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTAGGGGCCAAAAGAGGCTCTGTAACGAGACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCTCTACCCAAAAGTCAAATTTAGTCAAGCATTTACCAACAAACAGG
CAGAGTTCATTTCTATCTGCCATTAGACCTTCTTATCATCCATCACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKSGKTSCKDNKLNVSFVRVLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
CAACCTGGATATTCTGAGACATATTTTGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCTT
CCATTTAGAGTGTAGCAAAGGAAAAAACCAAGGTTGGGTTCTTCTGACATTGGCAGTG
CCCCAGTAGGGGTGGGATGAGCGAATATTCCAAAGCTAAAGTCCCACACCTGTAGATTAC
AAGAGTGGATTTCGAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
ACCACGTCTTGGAATTTAGTGGGTCTTGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
GAGAGGAGGGAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGTTGGATCCACTGAGG
AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACCTGGCTGCT
GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGCAG
CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
CGCGCTCCGGGCGCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGTATGCGGCGCTGGC
CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTCTGG
CGCAGCGGCGCTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCTTG
CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGGCCGACCGCGGCCCGGAGCCTCA
GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCAGATCCCT
ACGGAAGCATCCAGGGCAGCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT
GTGGGCTCCGTGTGGTCACCATCCAGAGCGCAAGCTGGGTCACTACATGGCCATGAATGC
TGAGGAGTGTCTACAGTTCGCGCATTTTCACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
TTGAGAATTACTACGCTCTGTACGCTCTGCTCTCTACCGCCAGCGTCTGTTCTGGCCGGGCC
TGTGACTCTGGCCTGGACAAGGAGGCCAGGTCATGAAGGGAACCGAGTTAAGAAGACCAA
GGCAGCTGCCACTTTCTGCCGCAAGCTCTGGAGGTGGCCATGTACAGGAGCCTTCTCTCC
ACAGTGTCCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCCCTGAAATGTAGTCCCTGGACTG
GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIQKREVRPPGSGRPVSAQRVRCPRGTSKLCQKQLILLISKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYIQANPDGSIQGTPEDTSSFTFNLIPIVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

ATGCGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCAGCTCAAGGTTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCGATGGAGTCTCTCATGGAACCAAGGATGACAGCCTAATTTCTACACTCT
TCAACCTCATACCACTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAATAAGGAAGGCGCAAGCTATGAAGAGGGAACAGA
GTAAAGAAACCAACACAGCAGCTCATTTCATCCCAAGCCATTGGAAGTTGCCATGTACC
AGAACCATCTTTGCATGATGTTGGGGAACCGGTCCGAAGCCTGGGTGTACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACATAG

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWD RPSASRRSSPSKNRGLCNGNLVDIFS KVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGALDGTKDDSTNSTL FNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

GGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCGTTGCAAAAAAT
GAAGGATCGAGGACGCGAGCTTTCTCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAGGAAGA
ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAAACACAAATGTGTATATGTGCACACAGGGGACATTCAAGATAT
ATAATAAACACAGAGTTAGACCGCGGGGGTGGTGTGTTGTGCACATAATAATAATCTTAAAGACGCTGTCC
CTCCCCACCCCAAAAAAAGGATGATTGGAATGAGAACCAGGAGATTACAAAAAAGTAATGTCTATT
TTCTCTATAAAGGAGAAAGTGAGCCACAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTAGTAAAGTAA
AGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAGAGGAGAGAAATATATAATACATCTGC
AAGAAATTTTCAGAGAGAAAGAAATGACCCGGCAGATTGAGGCATGATTGGGGGAGAACACGACGACGCA
CAGTTGGATTTGTGCGTATGTTGACTAAATGACGAGATAATGCGATTGGATTTTCTCATCAACCCCTTT
TTTTTAAATTTTTATCTCTTTGGTATCAAGATCATCGCTTTCTCTGTTCTTAACCACCTGGATTTCATCT
GGATGTGCTGTGATCAGTCTGAATACAACCTGTTGAATTCAGAGAGGACCAACACGAGATAAATTGATGATG
TTGAACAAGATGACCTTACATCTGACGACAGATAAATGATAGGCTCTAGTTTAAACAGGGCCCTATTGACCCCT
GCTGTGGTGTCTGCGCTCTTCAACTTGTGGTGGCTGGTGTGGTGGCGGCTCAGACCTGCCCTCTGTGTT
GCTCCTGCAGCAACCAAGTTGCAAGAGGTGATTGTGTTGGAAAACCTCGTGAGGTTCCGAGTGCGATCTCC
ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG
GCACTTGGAATCTCAGACTTGAGTAGGAACCATATCAGAACCAITGAATTTGGGGCTTCAATGGTCTGGCGA
ACCTCAACACTCTGGAACCTTTGCAACTGCTCTTACTACCATCCCCAATGGAGCTTTTGTATACTCTGTCTAAA
CTGAAGGAGCTCTGGTTGCAAAACACCCCATTTGAAAGCATCCCTTCTATGCTTTTAAACGAATCTCTCTTT
GCGCGGACTAGACTTAGGGGAATTGAAAAGACTTTATACATCTCAGAAGGTGCCTTTGAAGGCTGTGCCAAT
TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGGAATCCCTAACCTCACACCGCTCATAAACATAGATGAG
CTGGATCTTTTGGGAATCATTTATCTGCCATCAGGACTGGCTCTTTCCAGGGTTTGATGACCATCTCAAACAT
GTGGATGTACAGTCCGAGTTTCAAGTGAATGACAGGATGCCTTGACACCTTCAGTCACTAGTGAGGATCA
ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
TTACATCACAAACCTTGGAACTGTAATCTGTACATACTGTGGCTCAGCTGGTGGATAAAGACATGCCCCCTC
GAACACAGCTTGTGTGCGCGGTGTAAACATCTCTCCCAATCTAAAGGGGAGGTACATTTGAGAGCTCAGCCAGA
ATTACTACATGCTATGCTCGGTGATTGTGGAGCCCTCGACAGCTCAATGTCACTGAAGCGATGGCAGCT
GAGCTGAAATGTGGGGCTCCACATCTCTGACATCTGTATCTTGGATGATCCAAATGGAACGATCATGACATA
TGGGGCGTACAAAGTCGGATAGCTGTGCTCAGTGATGGTACGTAAATTTCAAAATGTAACGTGTGCAAGATA
CAGGCATGTACACATGTATGTTGAGTAATCCGTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
GCAACCTACTCTCTTCTCTTACTTTCAACCGTCACAGTAGAGACTTGAACCGCTCTCAGGATGAGGACG
GACCCAGATACAAATGTGGGTCCACTCTCAGTGGTCACTGGAGACCAATTTGTGACCATCTCTCTCACAC
CACAGAGCAACAGGTGCGACAGAGAAAACTTCCACATCCCGTGACTGATATAAACAGTGGGATCCAGGAATT
GATGAGGTGATGAAGACTACCAAAATCATCTATTTGGTGTTTTGTGGCCATCACACTCATGCTGCACTGATGCT
GGTCATTTCTACAAGATGAGGAAGACGACCATCTCGGCAAAACCATCAGCGCCCAACAGGAGCTGTTGAATTA
TTAATGTGGATGATGAGATTACGGGAGACACCCGATGGAAGGCCACCTGCCCTGCTGCTATGAGCATGAG
CACCTAAATCTACTATAACTATACAAATCTCCCTCAACGACCAACACAGCAATTAACATAAATTAATCAATA
CAGTTCAGTGCATGAACCGTTATTGATCCGAATGAACCTCTAAAGACAATGTACAAGAGACTCAAACTTAAACAA
TTTACAGAGTTACAAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAATGATGGGGCTAA
ATCTACTGTTTCAAAAAAGTCTCTTTACAAAAAACAAAAAGAAAGAAATTTATTTATTAATAAATCTATTG

MLNKMTHLPQQIMIGPRFNRLFDPLLVLALLQLLVAVGLVRAQTCPSVSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSEFKHLRHLLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNPIESIPSYAFNRIPSLRRLDGLGELKRLS
YISEGAFEGLSNLRVYLNAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHPDLFTPLHHLERIHLHHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVGN
TTASATLNVTAATTTFSYFSTVTVETMEPSQDEARTDNNVGTPVVDWETTNVTTSLTPQ
STRSTKTFITIPVTDINSIGPIGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRQHHHRQN
HHAPKRTVEIINVDDEITGDTFMESHLMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHS
VHEPLLIRMNSKNDOVETOI

amino acids 1-44

amino acids 523-543

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

amino acids 183-187

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

CGCCCGGGAGGCCAATCTGCCCCAGGGGACAGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
GGCTCGAGCCACCTCTCGCGCGCACCCGAGGCGCGCGCCAGCTCGCCCGAGGTCGCTCGGA
GCGCCCGCGCGCCCGGAGCAAGACGAACTAGCGGGGAAGCGCCCGCTCGGGGATC
GGG**ATG**TCCTCCTCTCTCTCTCTCTTGTCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGGAGAAAAGGCTACTTTGCCCTGACCCACTCACTGGGGC
TCCGAAAAAGACACTCTGGATAGTTAATGGTCTACCAGATAATGAAGGAAACCAAA
GTGGTGATCACTTACTCAGTCTGCTGATGTCTACAATACTTGACTGAGGAACAAGGGCC
ATGGCCCTTTGCTTCCAATTTCTCTGCAAGGATGCTCTCTGAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCGCGGTACACCTGTAAGGTTAAGAATTACGGGCGTACGTGTGGAGCAT
GTCATCTTAAAGTCTTTAGTAGGACCTCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTCGAGTGTAGTCACTCTCGGCACAGAGCCATTGTGTATT
ACTGGCAGCGAATCCGAGAGAAGAGAGGTGAACGCTCTGCTCCCAAATCTAGGATT
GACTACAAACCCCTGGACGAGTTCTGGTGAGGAATTTACACTGTCTCTCTGGACTGTGTA
CGAGTGACACAGCAGGCAACGAAGCTGGGAAGAAAGCTGTGTGGTGCAGTAGTGTACAGT
ATGTACAAGCACTCGGCATGGTTGTCCAGGAGCAGTGCACGGCTATGTGGCTGGAGCCCTGCTG
ATTTCCTCTTGGTGTGGCTGCTAATCCCAAGAAAGACAAAGAAAGATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCGCTCTGTGAAACCCAGCT
CCTCTCTCTCAGGCTCTCGGAGCTCAGCTCTGTGGTTCTCTCTCCACTCTCGCTCCACAGAAAT
AGTGGCTCAGCGACGCCACGGACATGCTCACTGACGACAGCCACCCAGCGAGGCTGGCCAC
CCAGGCATACAGCTCTGTGGGGCCAGAGGTGAGAGGCTGTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAAACCAACCCAGCATGATCTCCCGAGCCAGAGCAGAGCGTTCCAA
ACGGTCT**TGA**ATTACAATTGCACTTGACTCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
TCTTCGTCTATTGGAGCTCAAGTCAACAGGCCACACAACCAAGCTATAGAGGTCCTCTAAGTAGCA
GTGAGCATTGACCGGAACGATTTCAGATGACATTTCTTATATACAATACCAACAGCAAAA
AGGATGTAAAGCTGATTTCATCTGTAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTGCMAATCTATTGTTCAGCAGGACCTCTGGTGAGAAGTTGGGGAAAGGGT
AGGTAATATACCTAAACCTTTAATGTGGGATATTTTGATCATAGTGGCTTTGATTCACAAAT
TTCAGAGGAATATGGGATGCTGTGTTGTAATTTTCTATGCAATTCGCAAACTTATGGATT
ATTAGTATTACAGAGTCAAGCAAGCAACCCAGCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACTTCTAAGAAACTCCAAAAAAGGAACATGTGTCCTCTATTCTGACTTAAC
TCTATTGTGCTAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGTAGGAGA
AGAGTAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAC
TATGAAGGAGACAAAAATTTGTGACAAAGGATGTGTAAGAGCTTTCCATCTTCATGATGTT
ATGAGGATTGTGACAAACATTAGAATATATAATGGAGCAATGTGGATTTCCTCCCTCAAA
CAGATGCTCTAAGGACTTCTCTGCTAGTATTCTTGAAGAGAGAAATACAACTATGTCATT
TCTCAACGTCCTTAGAAGAAATCTCTTAGAGAAAAGGGGATCTAGGAAGTCTGAAGAGATTA
CCCAACTACATTATATAGTCTCTCTCTCTAGAAAAATGTGAACCCAGAAATGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCGGGCA
TGGTGGCAGGCCCTGTAGGAAATCCAGCAGTGTGGAGTTGCACTGAGCCGAGATTATGCC
ATTGCACTCCAGCTGGGTGACAGAGCGGACCTCGCTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELETGSDLTLCQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQFGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFAQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSTTPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQDCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLSGMSPSNM
EGYSKTQYNQVPSEDFERTFPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCATGCCTCTGATTGGTGA
ATGGTGAAGGTGCCTGTCTAACTTTTCTGTA AAAAGAACAGCTGCCTCCAGGCAGCCAGCC
CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
CAATTTAACACCAAGAAGATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCGCCCTG
CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCTGGGTTTTACCTG
CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
GAAGGGGGTTGTTCCCGAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAGACACTATGCAAG
CTCAGGATAACATCACGAGTGCCCGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCCTCGGAT
GCTGAGAGCTGTTACCTTGTCCACACCTGCTGGAGTTCTACTTGAAAACGTGTTTTCAAAAA
CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACCT
TGTTCTCTCATCGTGCTCAACCTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
AGTGCAACACGGCGTTTTCTGCTATCTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
TCTGACCAAAGCCCTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGCAAAATCTACAAG
TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCATTGGTTGTGCTCTGTCATTCTCA
AACAGTCTCCCTTCTATGCTGTTCACTGGACATTCACGCCCTTGCCCATGGTGTCCTATTTC
TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTTATTACAACCTCTATTT
AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
CAGCAGAATATTGTGCCCCATGCTTCTTTACCCTCACAATCCTTGCCACAGTGTGGGGCAG
TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
GTTAAAAAACAGAGAGGGATGCTTGATGTA AAACCTGAACCTCAGAGCATGAAAATCACACT
GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGTGCACTGTGTTGAAAAG
TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCCTAATAAAACATTTCAATT
TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTCCCTTGGTGCCCTCCTTTTTTTTT
TATCTCTAGTCATCTTCCCTAATCTTCCACTTGAGTGTAAGCTGACCTTGCTGATGGTGAC
ATTGCACTGATGTACTATTCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
CTCCAAAAA AAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLLSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLYLKTIVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRLFLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCCAAATGTCATATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCA~~ACT~~CCTTTCTCTACA
TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

CCCGTGCCAAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTTGCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACGTGCACCT
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGC**ATG**TTGGGGGCCGCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
ATGCTCCCCACTGCTCGGCTCCAGTGGGGTGGCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGCCATGTGGATGGCGACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTGGATCACACTATTTTGAC
CCGGAGAACTGCAAGTTCCAACACAGACGCTGGAAAACGGGTACGACGCTTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCTCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCGTAACGT
GCTGAAGCCCCGGGCCCGGATGACCCGGCCCCGGCTCCTGTTACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGCGGTCGAGTGAAC
ACGACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATC**TAG**GGTCTG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYL CMDFRGNIFGSHYFDPENCRFQHQTLNGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPYPYSQFLSRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGTCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGACCCGGGCCACGCCGCTCTGGAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCCGAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTACAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTGACCCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCGCTCACGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
 GTCACGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTAT
 GGTCGCCGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTACAAACATCGAG
 GTTATTAATTCAGCATCACAGAAATAGAAACAACACTTCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCCTCGTCCACCTCCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTCACAGCCTCTGCCGAGACCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGCTCTCCATAGAGGCTGGGTGAGTGGGCAAAACAACCTC
 CTTTGCTGGGAGCTCTGCTTCTCTTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCAACC
 CTTAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCTT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGACG**TGA**TGTCAGGTGAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGCTGCTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGAGGGGCTTCACTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCACTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCCTGCA
 TTAAATTAACCTCAGTGTGGCCCAAAAAA

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALQTLSA
ETSSRASTPAGPIPEAETRGAKRISPARETRSFKTSPNFMVLIATSVETSAASGSPGAGM
TTVQITITGSDPEEAFDFTLCTDSSSEAKLTMDILTLAHTSTFAKGLSSESSASSDGPHFV
ITPSRAESSASSDGPHFVITPSRAESSASSDGPHFVITPSWSPGSDVTLAEALVTVTNI
EVINCITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
STAGTSEASAPHATVGTPLPTNSATEREVATAPGATLTSGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSEIAGSAGKTTTSFAGSSAGSPSEALKNFTPSRPTMTDIATKGFFPTSRD
PLPSVPPTTNSRGTNSTLAKIITTSAKTTMKPOOPRPLRPGRGROT

amino acids 252-256, 445-449, 451-455

amino acids 84-90

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169, 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339, 404-408, 414-418, 431-435

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-320, 349-355, 386-392, 397-403, 449-455

amino acids 385-393

CGGAGCATCCGCTCGCGTCTCGCCGAGACCCCGCGCGGATTTCGCCGGTCTTCCCGCGG
GCGCGACAGAGCTGCTCTCGACCATCTGGATGGCAGCAGGGCGCCCGGCTCTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGACGGCTTTCTAAAGCAAATCAAGGACGAGGGAGATTAT
CCTTGACCTTTGAAGACCAAACATAAAGTAAATTTAAATGCTTCTTCGGGGGAGAAGGGAG
CTTGAGTTCACACTTTGGTAAATAATTTGCTCTCTGACATCAAGCTGTCTGCTAGTCAAGAAAT
GCCTCAAAAAGAGTCTAGAAGATGTTGTCTATGACATCAGTCACTCTCTTTTCAAGGGAATC
AGAGGCAATCTGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATCTTGTGTTCAAC
AAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGACATCGAAAAACAGTCA
GCAACCCAACTGCTACTAATTTTCTGCTCCCAACGAGGAAGCTGTCCATTGAACACGCA
AAAGAGCTTATGAGTTACAGGATAATACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
CCAAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAAATTTCAAGAGCACTCACTCCC
TAGCCCATCATCACAGAGATTATCAAAGCCACCGATATCATGACGAGACACATCTTCT
CAGAAGTTTGGATCTCATGATCAAGCTCGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
GCTCTTGTCTTATAGGAAAAAAGGCCATCTCAGAGTTCAACAATTTTCTCTGTATCAAGAA
TAGCTCATCTGCTGCTGAAAATGTAGTGGCTGCCAGTACGGTGGCAGTGGCTCTTCCA
CATACCACTCGGCTACTCCAAGCCCGCACCTCTTACCACCAATGCTTCAGTGACCC
TCTGGGACTTCCAGGCCACAGCTGGCCACCAACAGCTCCACCTGTAAACCTGTCACTTCTC
AGCTTCCACGACCTCTATTCTACAGTTTTTACAGGGCTCGGGCTACATCCAAGCAATG
GCTACCAACAGCAGTGTCTGACTACCACTTTTACAGGCATACCGGATCGAAAGGACGCTTGA
AACCATACCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGAATGTGTATAACCTA
CTGCACTTCTATGTCAAATGTGGAGTCTTCCATATGAATAAACTGCTTCTGGGAAGGT
AGGGAGGCCAGTCCAGGCAGTCTTCTCCGAGCGAGTGTTCAGAAATCAGTACGCCCTTCC
ATTTGAAAATGGCTTCTATCGGGCTGCTGCTCTTGGTGTCTGCTCTGGTATAGGCC
TCGTCTCTCTGGGTAGAAATCTTCTGGAAATCACTCCGACGGAACGTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATTAAGGATGAACTCGGTGTCTCTTAATCATT
TAGTAAACAGAAAGCCAAATGCAATGAGTTTCTGCTGACTGCTAGTCTTAGCAGGAGTGT
TATTTTGAAGACAGGAAATGCCCTCTGCTGTTCTCTTTTTTTTTTGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTACCCGCAACCTCGCTCTC
CTGGGTTCAAGCGATTCTCTGCTCAGCCCTCAAGTATCTGGGATACAGGCATGTGCCA
CCACACTCGGGTGATTTTGATTTTTATGTAGAGACGGGGTTTCCACATGTGGTCAGGCTG
GTCTCAAACTCTGACCTAGTAGTATCCACTCTCTGGCCTCCAAAGTGTGCGGATTACAGG
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGGAGAAGGAATGAAGTG
GGAACCAATTAAGTAAATTTGGGTAAATCTGCTCTAAATATAGCTAAACAAAGCTCT
ATGTAAAGTAATTAAGATAAATGGCATATAAATTTCAAATTAACATGCTTATGTCAA
GAACACAGGTTAGACATATGAGTTTCCAATTCATTCACATTTCTGGTTCAGATAAAATCAAC
TGTTTATATCAATTTCTAATGGATTTGCTTTTTCTTTATATGGATTTCTTTAAACACTTATT
CCAGATGTAGTTCTCTTCCAATTAATATTTGAATAAATCTTTGTGTTACCA

FIGURE 328

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><subunit 1 of 1, 431 aa, 1 stop
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MFFGEGSLTYTLVLCFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGI RGN E P V Y T S T Q E D
C I N S C C S T K N I S G D K A C N L M I F D T R K T A R Q P N C Y L F F C P N E E A C P L K P A K G L M S Y R I I T D F P
S L T R N L P S Q E L P Q E D S L L H G Q F S Q A V T P L A H H H T D Y S K P T D I S W R D T L S Q R F G S S D H L E K L F
K M D E A Q L L A Y K E K G H S Q S S Q F S S D Q E I A H L L P E N V S A L P A T V A V A S P H T T S A T P K P A T L L
P T N A S V T P S G T S Q P Q L A T T A P V T V T S P T T L I S T V F T R A A T L Q M A T T A V L T T F Q A P
T D S K G S L E T I P T E I N L T L N T N V N P T A L S M N V E S S T M K R K R Y S R L D Y L I N G Y V D I

amino acids 1-25

amino acids 384-405

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

amino acids 415-419

amino acids 50-57

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCAGAA**ATG**CGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACACCAGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGGCCAGGAGCAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTACCTTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCTGCTTTCCAGGACCTGCTGTCTCCCTCCCTCTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCTGCAGCCAAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCATTTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCTACCCAGCGACCTCTCTCTCTGACGGGAGCTCCCGCCCCCATGACAG
 TGGACTCCACCTCAGCAGAGGACACCAAGTCCAGTCTCAGCAGTGGCAGCTCTAAGCCGAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCCTGGTGTGCTGAGCCTTCTGTGAGC
 CGCAGGCTGATCGCCTCTGTCAGCCACCTGCTCTCTGTGGAGAAAGGAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAAAGTTCTGGCTCTCAGCCTTACTGCGGAGGAAAGGAAGCC
 CCTTCCAGGCCCTGAGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCG**TAG**GGCAGGAGGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATCGCTGGCTGGATCAGCACCAGTTCGCCAAAGCTTCCACCTCAGCCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTTCCCGAGGCTCTCTCTTGGATGTTCCA
 GCCTGACCTAGAACGCTTTGTCTCAGCCCTGAGGCCAGCGGCTGCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCTATGCCAGTGTCTGGACCCCTGCCTTCTCCCACTCCAGACCCCACTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCAGGCTCTCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCT
 GGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCAACAATGCCCACTGACTGTGCACTTGAGTTTGGGGCCAGTGGGCCCTG
 ATGAACGCTCACACCCCTTCACTTAGAGTCTGCATTTGGGCTGTGACGCTCTCCACTGCC
 CAATAGATCTGCTCTGCTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTCAGGTGCACATTTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCTTTNCCATTTGCCCTCCTGGNCCATGCCTTCTTGCCTTGGAAAAATGATGAAGA
 AAACTTGGCTCCTTCTTGTCTGGAAGGGTTACTTGCCATATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAAACAGAGTGACGTAGGTCTTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGGGGGTGGTGAAGTA
 GCACAACCTACTATTTTTTTCTTTTTCCATTATTATTGTTTTTAAAGACAGAATCTCGTGCT
 GCTGCCAGGCTGGAGTGAGTGGCAGCATCTGCAAACTCCGCTCTCTGGGTTCAAGTGATT
 CTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGCTTTGAACCTCTGAC
 CTCAAATGAGCCTCTGCTTCTAGTCTCCCAAATTGCGGGATTACAGGACAGCCACTGTG
 TCTGGCCCTATTTCTTTAAAAAGTGAATTAAGAGTTGTTGAGTATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTCAACCATAGTCTACCCAGAGACTATCAT
 TATTTCTGTTTTGTTGTAAGTCTCTTCCACTCTTTTCTTCTTACATAAATTTGCGGGTGTCTT
 TTTACAGAGCAATTATCTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTTCCAGCACTTCTGTGTTTACAGACCTTTTTATAAATAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPPEISGFEGDTVSLQCTYREELRDHRKYWCCKGGILFSRCS
GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDAGEYWCWVEKRGPDSELLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGGTGAEEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEEAPSQAPEGD
VISMPPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128